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GenCore version 5.1.6
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November 16, 2004, 16:34:37; Search time 40 Seconds (without alignments) 1096.871 Million cell updates/sec Run on:

US-09-905-589A-2 2364 1 MRKISNHGSLRVAKVAYPLG.....ALGAIFHYIDSLNRQKSPAS Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		a <b>k</b> o			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	590.5	25.0	479	2	T23508	hypothetical prote
7	508	21.5	556	7	T39109	probable quanogine
3	498	÷.	518	7	A40732	quanosine-diphosph
4	485	20.5	454	(1	JC4616	apyrase (EC 3.6.1.
ហ	442.5	8	455	7	S48859	nucleoside triphos
9	372	'n.	516	N	G84442	probable nucleosid
7	343	14.5	485	7	T34147	hypothetical prote
80	339.5	14.4	483	~	D86276	
σ	329.5	13.9	3	~	S50463	
10	307	13.0	557	7	T16696	
11	301	12.7	405	~	E86276	
12	285.5	12.1	510	~1	156242	_
13	281.5	11.9	572	~	T40856	probable nucleotid
14	245.5	10.4	1052	7	T04439	hypothetical profe
15	219	9.3	508	7	C86276	7A19.33 protein -
16	140.5	5.9	628	N	A55421	nucleoside-triphos
17	111	4.7	619	7	C71007	probable formate d
18	108.5	4.6	1186	ď	T12737	tail protein - Met
19	106.5	4.5	665	N	E75124	formate dehydrogen
20	104.5	4.4	322	7	T24948	hypothetical prote
21	103.5	4.4	322	7	T27308	hypothetical prote
22	102.5	4.3	440	7	139847	cell-division prot
23	102	4.3	475	N	G72274	glutamyl tRNA-Gln
24	102	4.3	623	Ŋ	G81346	heat shock protein
25	102	4.3	4162	7	T42633	connectin/titin -
26	100	4.2	1233	7	T37045	nitrate reductase
27	100	4.2	26926	٦	I38344	titin, cardiac mus
28	99.5	4.2	470	٦	38	dihydrolipoamide d
29	•	4.2	504	7	S17724	H+-transporting tw

dnaK-type molecula	tyrosine kinase su	DNAK Protein limpo	dnaJ protein (heat	adenosylhomocystei	triacvîglycerol li	actinomycin synthe	probable efflux pr	DNA topoisomerase	hypothetical prote	hypothetical prote	protein W03D8,9 [i	heat shock transcr	triacylglycerol li	cvclosporin synthe	nicotinic acid pho
I39585	A46299	AE2591	E97373	C64473	832615	T14591	T35970	873898	T25894	T32940	D87733	S25478	S2344B	841309	F97119
N	7	N	~	Н	7	7	7	~	~	N	N	Н	N	~	~
633	2411	633	633	415	548	2611	815	711	1217	325	325	527	549	15281	489
4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.1	4.1	4.1	4.0	4.0	4.0	4.0	4.0	4.0
99.5	99.5	98.5	98.5	97.5	97.5	6	96.5	96	96	95.5	95.5	95	95	95	94.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1 T23508 Hypothelical protein K08H10.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T23508	submitted to the EMBL Data Library, November 1996 A;Reference number: Z19750 A;Accession: T23508 A;Accession: T23508 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Btatus: preliminary; translated from GB/EMBL/DDBJ A;Btatus: preliminary; translated from GB/EMBL/DDBJ A;Expecine type: DNA A;Residues: 1-479 <wil> A;Residues: 1-479 <wil> A;Experimental source: clone K08H10 C;Genetics:</wil></wil>	A;Gene: CESP.K08H10.4 A;Map position: 5 A;Introns: 36/3; 83/3; 189/1; 300/2; 412/3 C;Superfamily: nucleoside triphosphatase chromatin-associated
RESULT 1 T23508 hypothetical protein C; Species: Caenorhal C; Date: 15-Oct-1999 C; Accession: T23508 R; Gardner, A.	submitted to the EMBL Data A;Reference number: 219750 A;Accession: T23508 A;Status: preliminary; trai A;Molecule type: DNA A;Residues: 1-479 <mil> A;Cross-references: UNIPRO' A;Experimental source: clo C;Genetics:</mil>	A;Gene: CESP:KOBH10.4 A;Map position: 5 A;Introns: 36/3; 83/3 C;Superfamily: nucleo

. б 73 FYGIMFDAGSTGTRVHVFQFTRPPRETP----TLTHETFKAVKPGLSAYADDVEKSAQG 127 187 CVSIMNGTDEGVSAWITINFLIGSL-----KTPGGSSVGMLDLGGGGSTQIAFLPRV 237 356 YYYDLAAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSS----PFSCMDLTYV-SL 410 238 EGTLOASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPC 297 298 LSPSFK-GEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQ-NRVHRTEEVKHVDFYAFS 355 Gaps 25; Query Match 25.0%; Score 590.5; DB 2; Length 479; Best Local Similarity 34.2%; Pred. No. 4.4e-40; Matches 134; Conservative 78; Mismatches 155; Indels 25 222 g 엄 ð Op 8 g ð g à  $\delta$ g

ò g C.; Wei, Y.; Taylor,

P.; Komp,

9871. and

8334,

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A; Cross-references: EMBL: U18779; NID: 9603625; PIDN: AAB65000.1; PID: 9603637; MIPS: YEL042w
                                                                                                                                                                                                                                       A;Residues: 1-518 <MUL>
A;Cross-references: GB:U18779; EMBL:L10830; NID:g603625; PIDN:AAB65000.1; PID:g603637 R;Dietrich, F.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 EKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGIRLLPGEKAQKLLQKVKE-VFKASP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Keywords: glycoprotein; Golgi apparatus; hydrolase; transmembrane protein
F;10-24/Domain: transmembrane #status predicted <TMM>
F;41,280,335/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 VGAANSLDPLLKVAMNYVPIKARSCTPVAVKATAGLRLEGDAKSSKILSAVRDHLEKDYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F-LVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGS--SVGMLDLGGGSTQIAFLPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 FPVVEGDGVSIMGGDEEGVFAMITINYLLGNIGANGPKLFTAAVFDLGGGSTQIVFEPTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 TAADGHEVFYGIMFDAGSTGTRVHVFQF---TRPPRETPTLTHETFKAVKPGLSAYADDV
extracted from NCBI backbone (NCBIN:134708, NCBIP:134711)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.1%; Score 498; DB 2; Length 51 33.1%; Pred. No. 1.7e-32; tive 60; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, December 1994
A,Description: The sequence of S. cerevisiae cosmids 8199,
A,Reference number: S50491
                                                             A;Molecule type: protein
A;Residues: 125-144;238-257;276-281;366-374;399-412 <AB2>
R;Mulligan, J.T.; Dietrich, F.S.; Hemnessey, K.M.; Sehl,
submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: SGD:GDA1
A;Cross-references: SGD:S0000768; MIPS:YEL042w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRKIDNVETSWALGA 440
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                                                                                                                                                                                         A; Reference number: S30812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Description: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-518 <DIE>
                                                                                                                                                                                                                             A;Accession: S30837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S50502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 5L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Function:
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Matches
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A40732
guanosine-diphosphatase (EC 3.6.1.42) - yeast (Saccharomyces cerevisiae)
MyAlternate names: protein YEL042w
C;Species: Saccharomyces cerevisiae
C;Becies: Saccharomyces
C;Accession: A40732; Mandon, E.C.; Hausler, A.; Moremen, K.; Hirschberg, C.B.;
J. Call Biol. 122, 307-323, 1993
A;Accession: A40732; MUID:93308137; PMID:8391537
A;Accession: A40732, MUID:93308137; PMID:8391537
A;Accession: A40732
A;Accession:
                                                                                                                                                                                                                                                                                                        A; Accession: T39109
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL; All 21741; PIDN: CAB57338.1; GSPDB: GN00066; SPDB: A; Experimental source: strain 972h-; cosmid c824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 VAKQDIPFDFWKATPLVLKATAGLRLLPGBKAQKLLQKVKEVFKAS-PFLVGDDCVSIMN 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --SSVGMLDLGGGSTQIAFLPRVEGTLQASPPG- 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 VRPCSFNGVHOPKFTETFTDSPIYLISYFYDRMISLGM-----PSTFTIEDMKYLANSVC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----RILETQPQSSPPSCMDLTY-VSLLLQEFGFPRSKVLKLTRKIDN 431
                                                                                                                               probable guanosine-diphosphatase - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 E;Accession: T39109 E;Accession: T39109 E;Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D. submitted to the EMBL Data Library, October 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LAILGGVEGQPAKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 KELVSPCL-----SPSFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NRVHR---TEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIAAKYVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.5%; Score 508; DB 2; Length 55 32.4%; Pred. No. 2.8e-33; ive 66; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 YLTALRMFNRTYKLYSYSYLGLGLMSAR-
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142; Conservative
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Best Local
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A,Gene: SPD
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291
                                                                       PINEKMVDGEHKFDLKFGDENYTLYQFSHLGYGLKEGRNKVNSVLVENALKDGKILKGDN 319
                                                                                                                                                                                                                           320 TKTHQLSSPCLPPKVNATNEKVTLESKETYTIDFIGPDEPSGAQ------CRFLTDEI 371
                                                                                                                                                                                                                                                                                                                        LQ------NRVHRTEEVKHV----DFYAFSYXYDLAAGVGLIDAEKGGSLVVGD 379
                                                                                                                                                                                                                                                                                                                                                                                                     372 INKDAQCQSPPCSFNGVHQPSLVRTFKESNDIYIFSYFYDRTRPLGM-----PLSFTLNE 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----QPQSSPFSCMDLTY-VSLLLQEFGFPRSKVLKL 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apyrase (EC 3.6.1.5) precursor - potato
N'Alternate names: adenyl'pytrophosphatase; ATP-diphosphohydrolase
C.Species: Solamum tuberosum (potato)
C.Species: Solamum tuberosum (potato)
C.Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                SGOKAAASLHELCAARVSEV
238 EGTLQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGK-----
                                                                                                                                                                    ----ELVSPCLSPSFKGEWE----HAEVTYRV-
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Conservative
                           C; Accession: S65147; S48859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           438 AVEAISAL 445
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A; Residues: 1-516 <STO>
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C;Accession: JC4616; PC4147

R;Anada, M.; Gudotti, G.

Biochem. Biophys. Res. Commun. 218, 916-923, 1996

A;Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from pot A;Reference number: JC4616; MUD:96158985; PMID:8579614

A;Accession: JC4616

A;Molecule type: mRNA

A;Residues: 1-454 cHAN>

A;Cross-references: UNIPROT:P80595; GB:U58597; NID:g1381632; PIDN:AAB02720.1; PID:g13816
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C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Superfamily: nucleoside tripholase; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;8-25/Domain: transmembrane #status predicted <TMM>
F;8-25/Domain: transmembrane #status predicted <TMM>
F;8-44-65/Region: actin-heat shock protein 70-hexokinase beta-phosphate binding
F;192-212/Region: actin-heat shock protein 70-hexokinase gamma-phosphate binding
                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 59-55;96-131;132-160;236-253;332-345 <HA2>
A;Residues: 59-55;96-131;132-160;236-253;332-345 <HA2>
A;Experimental source: tubers
A;Note: The authors translated the codon GCA for residue 215 as Gly
C;Comment: This enzyme belongs to a family of E-type ATPases, and it catalyzes
enzyme has nucleotide substrate specificity, divalent cation requirement, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 YABDPKAAANSLEPLLDGAEGVVPQELQSETPLELGATAGLRMLKGDAAEKILQAVRNLV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-ASPFLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KNOSTFHSKDQWVTILDGTQEGSYMWAAINYLLGNLGKDYKSTTATIDLGGGSVQMAYAI 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVEGTLQA----SPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELVSPCLSPSFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQ-NRVHRTEEVK--- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VWNGGGGDGQKNIHASSFFYDIGAQVGIVDTKFPSALAKPIQYLNAAKVACCTNVADIKS 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 AHSPLGTAADGHE-VFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTH-ETFKAVKPGLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 SNEQFAKAPQNEDGEPYVQQKHLMSKDYNLYVHSYLNYGQLAGRAEIF-------KASR
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31.9%; Pred. No. 1.6e-31;
iive 68; Mismatches 183; Indels
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Matches 138; Conservative
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nucleoside triphosphatase precursor, chromatin-associated - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

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C;Species: Arabidopsis thaliana (mouse ear cress)
C;Dacte: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C;Accession: G84442
R;Lin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N M.; Koo, H.; Moffer, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.; Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
                                                                                                                                                                                                                         PIDN:CAA83655.1; PID:g56361
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A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 YGIMFDAGSTGTRVHVFQFTRPPRETPTLTH-----ETFKAVKPGLSAYADDVEKSAQGI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 STYPFLDKKNVASYVCMDLIYQYVLLVD-GFGLDPLQKITSGKEIEYQDAIVEAAWPLGN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 RELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVF-KASPFLVGDDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 VSIIDGTQEGSYLWVTVNYALGNLGKKYTKTVGVIDLGGGSVQMAYAVSKKTAKNAPKV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ADGDDP-YIKKVVLKGIPYDLYVHSYLHFGREASRAEILKLTPRSP------NPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 LAGFNGIYTYSGEEFKATAYTSGANFNK------CKNTIRKALKLNYPCPYONCTFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------VDFYAFSYYYDLAAGVGLIDAEKGGSLV-VGDFELAAKYVCR-TLETQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 GIWNGGGGNGQKNLFASSSFFYLPEDTGWVDASTPNFILRPVDIETKAKEACALNFEDAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 VSIMNGTDEGVSAWITINFLIGSLKTPGGSSVGMLDLGGGSTQIAF-----LPRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 GTLQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCL
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable nucleoside triphosphatase [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                             455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 SPSFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLONRVHRTEEVKH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 516;
Filsieh, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.
Plant Mol. Biol. 30, 135-147, 1996
A;Title: Light-modulated abundance of an mRNA encoding a calmo A;Reference number: S65141; MUID:96197404; PMID:8616230
A;Molecule type: mRNA
A;Rossidues: 1-455 <HS2>
A;Cross-references: UNIPROT:P52914; EMBL:Z32743; NID:9563611; C;Superfamily: nucleoside triphosphatase chromatin-associated C;Keywords: nucleus
                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: nucleoside triphosphatase chromatin-associated
                                                                                                                                                                                                                                                                                                                                    Score 442.5; DB 2;
Pred. No. 4.6e-28;
9; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 372; DB 2
Pred. No. 3e-22;
                                                                                                                                                                                                                                                                                                         18.7%; Scur
29.2%; Pred
79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.7%;
29.0%;
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Best Local Similarity
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A;Map position: 2
C;Superfamily: nuc
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Aatches  1 1 1 1 2 2 SULT 7 4147  Pothetics Species: Species: Species: Species: Species: Crossines Crossines Cross-rept: Experimes Experimes Superfam: Super	a & a &	90 AV	RESU D862 C,Sp C,Da C,AC R,Th Chi.	A; Au Rizz A; Au	A P P P P P P P P P P P P P P P P P P P	Ma Ma	g &	영 &	g Å	g &	oy Oy	ov ov	<u>업</u>
	Aatches 113; Conservative 67; Mismatches 173; Indels 36; Gaps 1.  74 YGIMFDAGSTGTRYHVEQFTRPPRETPTLTHETPKAVKPGLSAYADDVEKSAQGIR 12    ::	127 ELVEFAKGRVFKGMMIEIEVRLMAIAGMKLEELEVQGKILGGVRKRVLGSGFEIRFADEMAN 190 IMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGTLQASPPGYL :::	RISEGNUTYNLYSHSFLHFGQNAAHDKLWGSLLSRDHNSAVETTRE-KIFTDPCAPKGY  KGBWEHAEVTYRVSGQKAAASLHELCAARVSEUQNRVHRTEEVKHVDFYAF  NLDANTOKHLSGLLAEES-RLSDSPQAGGNYSQCRSAALTILQDGNGRILIIIAGF  SY-YYDLAAGVGLIDAEKGGSLVVGDFEIAAKVCRTLETQPQSSPFSCMDLTY-VSLLL	QEFGFP-RSKVLKLTRKIDNVETSWALGA		P:C33H5.1	; yenecros: 8,Gene: CES: 8,Introns: 22/1, 83/1; 120/2; 167/1; 269/3; 399/3 2,Superfamily: nucleoside triphosphatase chromatin-associated	Зарв	HEVFYGIMFDAGSTGTRVHVFQFTRFPRETPTLTHETFKAVKFGLSAYADDV ::	EKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPF  : : :     : :     : : :   : :   : :   : :   : : :   : : :   : : :   : : : :   : : : : :   : : : : : : :   :	L-VGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT	LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELV 29 ::   : :	SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEV 33

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ture 408, 816-820, 2000
Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C., A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Z.O., M.; Rooney, T.; Rowley, D.; Sakano, H.

Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon, I. K., H.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

Reference number: As6141; MulD:21016719; PMID:11130712

Accession: D86276

Status: preliminary

Molecule type: DRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         esidues: 1-483 <STO>
ross-references: UNIPROT:Q9XI62; GB:AE005172; NID:g5080801; PIDN:AAD39311.1; GSPDB:GN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 KELVSPCLS--PSFKGEWEHA-----EVTYRVSGQKAAASLHELCA--ARVSEVLQNR 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 KNYSSGFLADESKLKGSLQAAGNFSKCRSATFALLKEGKENCLYEHCSIGSTFTPDLQGS 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 VHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSP 399
                                                                                                                                                                                                                                      388 CR----TLETQPQSSPF-----SCMDLTYVSLLLQEFGFPRSKVLKLTR---KID 430
                                                                                                                                                                                                                                                                             74 YGIMFDAGSTGTRVHVFQF----TRPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELLDVAKODIPFDFWKATPLVLKATAGLRLLPGEKAQKLLOKVKEVFKASPFLVGDDCVS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 VISGSDEGIYSWITANYALGSLGTDPLETTGIVELGGASAQVTFV----SSEHVPPEYS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TALRMFNRTYKLYSYSYLGLG-----KDG---LMSARLAILGGVEGQPA-----KDG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 RIJAYGNISYTIYSHSFLDYGKDAALKKLLEKLQNSANSTVDGVVEDPCTPKGYIYDTNS 303
                                                                                             -----LQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIAAKYV 387
                                                                                                                                                                 ----SGGEYHYQKFIDEVRKY 346
::| |:|| :
--DVCLAQVSSLIGDKAQP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             othetical protein F7A19.34 [imported] - Arabidopsis thaliana pecies: Arabidopsis thaliana (mouse-ear cress)
ate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uery Match
lest Local Similarity 26.5%; Pred. No. 1.2e-19;
latches 108; Conservative 78; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400 FSCMDLTY-VSLLLQEFGFPR----SKVLKLTRKIDNVETSWALGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uperfamily: nucleoside triphosphatase chromatin-associated
                                                                                                                                               292 SCPNPTCFLRNVIAPSVNLSTVQLYGFSEYWYTTSNFG-
: || : || 251 NDSCSPRGLNRLIGEFTVNGTGEW
                                                                                                                                                                                                                                                                                                                                                                                         431 NVETSWALGAIFHYIDSL 448
                                                                                                                                                                                                                                                                                                                                                                                                                             GEEMQWALGAMLYHSKDL 423
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RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 1816-820, 2000
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A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. A.Authors: Aggrence and analysis of chromosome 1 of the plant Arabidopsis.

A.Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 LLSKLKDQ---NGTVIQDDCMPLNL----HKTVTLE-NGENFVRRGTGNWNTCSNEVKK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 LINPESSSEVCKAEAAKCYFGAVPAPSIPLSNIEMYGFSEYWYSTHDVLGL-----GGQY 386
                                                                                                                                                                                                                                                                                                                                                                                   42
                                                                                                                                                                                                                                                                                                                  72
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 QGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLP-----GEKAQKLLQKVKEVFKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ::||::|:| | ::| | | | : | | | | : | | | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : : | : | : | : | : | : : | : | : : | : | : | : : | : | : : | : | : : | : | : : | : : | : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : | : : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 ASAQIAFELPDTDSFSSINVENINLGCREDDSLFK--YKLFVTTFLGYGVNEGIRKYEHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 ILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQ----KAAASLHELCAARVSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVGDFBIAAKYVC----RILETQPQSSPF-----SCMDLTYVSLLLQEFGFPRSK
                                                                                                                                                                                                                                                                                                                                                                                   --EAHTSPKVIADDOER
                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 FYGIMFDAGSIGTRVHVFQFTRPP-----RETPTL--THETFKAVKPGLSAYADDVEKSA
                                                                                                                                                                                                                                                                                                           13 AKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAHSPLGTAADGHEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFLVGDDCVSIMNGTDEGVSAWITINFL-----TGSLKTPGGS-----SVGMLDLGG
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                                                                A;Gene: CESP:R07E4.4
A;Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2
                                                                                                                                                                                                                                       88; Mismatches 178;
                                                                                                                                                                      Query Match
13.0%; Score 307; DB 2;
Best Local Similarity 23.5%; Pred. No. 6.5e-17;
Matches 119; Conservative 88; Mismatches 178
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Pred. No. 1.3e-16;
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Experimental source: strain Bristol N2
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25.4%;
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Best Local Similarity
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Best Local Similarity
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A;Status: preliminary
A;Molecule type: DNA
                            C; Genetics:
A; Gene: CESP: R07E4
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A;Molecule type: DNA
A;Residues: 1-557 <MIL>
A;Residues: 1-557 <MIL>
A;Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AAA80403.1; CESP:R07E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-630 <DIB>
A;Cross-references: UNIPROT:P40009; EMBL:U18778; NID:g603592; PID:g603597; GSPDB:GN00005
                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda
A;Reference number: S50433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLQKVKEVFK-ASPFLVGDDC---VSIMNGTDEGVSAWITINFLTGSLK--TPGGS---S 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGMLDLGGGGSTQIAFLPRVEGTLQASPPGYLTA-LRMFN---RTYKLYSYSYLGLGLMSA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 FGFWDWGGASTQIAFAPHDSGEIARHRDDIATIFLRSVNGDLQKWDVFVSTWLGFGANQA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R---LAILGGVEGQPAKD-----GKELVSPCLSPSFKGEWEHAEVTYRVSG----QKA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 RRRYLAQLINTLPENTNDYENDDFSTRNLNDPCMPRGSSTDFEFKDTIFHIAGSGNYEQC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 AASLHELCAARV----SEVLQNRVHRTE-EVKHVDFYAFSYYYDLAAGVGLIDAEKGGSL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 TKSIYPLLIKNMPCDDEPCLFNGVHAPRIDFANDKFIGTSEYWYTANDV----FKLGGEY 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            376 VVGDFEIAAKYVCRTLETQ-------PQS-SPFSCMDLTYVSLLLQE-FGFPRS 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein R07E4.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: Caenorhabditis elegans C;Date: 20-Sep-1999 #text_change 20-Sep-1999 (C;Accession: T16696 R;Miller, N. submitted to the EMBL Data Library, October 1995 A;Description: The sequence of C. elegans cosmid R07E4.
                                                                                                                                                       C.Species: Saccharomyces cerevisiae
C.bate: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 630;
                                                                                                                   hypothetical protein YER005w - yeast (Saccharomyces cerevisiae)
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R; Dietrich, F.S.
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A;Gene: SGD
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Db 334 NTSYCPYSQCENGIFLPPLGGDFGAFSAFYFWAKFLNLTSEKVSQEKV 382  Qy 377 VGDFEIAAKVCRTLETQPQGSPFSCMDLTV-SLLLQFFGFPRSKVLK 424    Db 337 TEMMKKFCAQPWEEIKTSYAGVKEKYLSEY-CFSGTVILSLLLQGYHFTADSWEHIH 438  Qy 425 LTRKIDNVETSWALG 433  RESULT 13  RESULT 13  RESULT 13  TAG0856  probable nuclectide phosphatase - fission yeast (Schizosaccharomyces pombe) C,Species: Schizosaccharomyces pombe C,Date: 0.0 - Dbol. 1999 #text_change 09-Jul-2004 C,Species: Schizosaccharomyces pombe C,Date: 0.0 - Dbol. T: Wood, V; Rajandream, M.A.; Barrell, B.G. R,Ramsperger, U.; Pobl, T: Wood, V; Rajandream, M.A.; Barrell, B.G. A,Rocession: T40856 A,Rocession:	Quary Match  Best Local Similarity 11-9%; Score 281.5, DB 2; Length 572;  Matches 111; Conservative 64; Mismatches 164; Indels 121; Gaps 15;  Matches 111; Conservative 64; Mismatches 164; Indels 121; Gaps 15;  A VINEDAGSSCRILITSH
Matches   104;   Conservative   65;   Mismatches   181;   Indels   60;   Gaps   13;   4   YGIMPDAGSTGTRVHVFOFTRPRETPTLITHETFRAVKPGLSAYADDVEKSAQGIRELD   133   4   FGWFESGRP   134   15   1   1   1   1   1   1   1   1	RESULT 12 196421 1796046 cell activation antigen - human 1796064 cell activation applies #text_change 09-Unl-2004 1796064 cell activation oz-Unl-1956 #text_change 09-Unl-2004 1796064 cell activation antigen. M.A.; Armitage, R.J.; Fanslow, W.C.; 1706064 cell activation antigen. Molecular cloning and structural chapter compact and activation antigen. Molecular cloning and structural chapter compact and cell experiments. 176212 deciration antigen. Molecular cloning and structural chapterial preliminary; translated from GB/EMBL/DDBJ 17060663 deciration antigen. Molecular cloning and structural chapterial cargo and cell experiments. 1707066 deciration antigen. Molecular cloning and structural chapterial cargo and cargo antigen. 1707067 deciration antigen. Molecular cloning and structural chapterial cargo and cargo antigen. 1707067 deciration antigen. 170707 de

119 124

Gaps

Indels 100; Length 508;

83; Mismatches 196;

299 283 335 343 391

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125 AQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVG 184
                                                                                                                                                                                                                                                                                                                                         120 SESVTELVEFAKKRVHKGKLKKSDIRLMATAGMRLLELPVQEQILDVTRRVLRSSGFDFR 179
                                                                                                                                                                                                                                                                                                                                                                             DDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGTLQAS 244
                                                                                                                                                                                                                                 GHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLT--HETFKAVK--PGLSAYADDVEKS
                                                                                                                                                                                                                                                        62 -VSLHYSVIIDGGSSGTRVHVFGY-RIESGKPVFDFGERNASLKLSPGLSAYADNPEGV
                                                                                                                                                          9 SLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAHSPLGTAAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 --LQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGD--FEIAAKYVCRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PSFKGEWEHAEVTYRVSG-----QKAAASLHE---LCAARVSEV---
                          A;Map position: 1
C;Superfamily: nucleoside triphosphatase chromatin-associated
                                                                                                                                                                                   | | : : : | | : : : | | 26 SKRTKSIIFVIVACVTIALGLLFIG------YSILRSGRNRR-
                                                                                  Match 9.3%; Score 219; DB 2; Local Similarity 22.3%; Pred. No. 8.3e-10; les 109; Conservative 83; Mismatches 196
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         R. Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Bancroft, I.; Mewes, submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15359
A;Accession: T04439
A;Accession: T04439
A;Molecule type: DNA
A;Residues: I-1052 <BEV>
A;Residues: UnIPROT:049676; EMBL:AL021687
A;Experimental source: UNIPROT:049676; EMBL:BAC clone T18B16
C;Genetics:
A;Map position: 4
A;Introns: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3
A;Note: T18B16.150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSQCASSVQGGKKGKSGVSIKLVGAPNWGECSALAKNAPCALPDGYPR----PHGQFYAV 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | SGFFVVYRFFNLSAEASLDDVLEKG-----REPCDKAWQVART-SVSPQ---PFIEQYCFR 885
                                                                                                                                                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S----YYYDLAAGVGLIDA-EKGGSLVVGDFEIAAKYVCRTLETQPQSSPF----SCMD 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 GVSAWITINFLTGSL-KTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMF
                                                                                                                                                                                                                                                                                                                                                                                                                                       543 INYKKDSSLPIVMKSLTEGISRKSRGRAYDRMETEPGFDKLVNNRTGLKTAİKPLIQMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 QDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYFGWTALNYQTSMLGALPKKATFGALDLGGSSLQVTF----ENEERTHNETNLM-LRIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 NRTYKLYSYSYLGLGLMSA-----RLAILGGVEGQPAKDGK-ELVSPCLSPSFKGEWE
                                                                                                                                                                                                                                                                                                                                     ----VFYGIMFDAGSTGTRVHVFQFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603 KQIPKNAHRTTSLFVYATAGVRRLRPADSSWILGNVWSILAKSPFTCRREWVKIISGTEE
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                  97;
                                                                                                                                                                                                                                                      10.4%; Score 245.5; DB 2; Length 1052; larity 25.3%; Pred. No. 1.6e-11; Conservative 60; Mismatches 185; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTYVSLLLQEFGFPRSKVLKLTRK---IDNVETSWALG 439
                                                                                                                                                                                                                                                                                                                               55 WGQQAHS-----PLGTAADGHE-
                                                                                                                                                                                                                                                                                                                                                                                                      ---RPPRETPTLTHETFKAV-
                                                                                                                                                                                                                                                                       Similarity
Accession: T04439
                                                                                                                                                                                                                                                                                           116;
                                                                                                                                                                                                                                                      Query Match
Best Local S:
Matches 116,
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completed: November 16, 2004, 17:00:26

Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chinson, M.F.; Hudghes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Ref. M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Edgence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: C86276

C86276
7AL9-33 protein - Arabidopsis thaliana
(C.Species: Arabidopsis thaliana (mouse-ear cress)
(C.Species: Avar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004)
(C.Accession: C86276

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-508 <STO> A;Cross-references: UNIPROT:Q9XI63; GB:AE005172; NID:g5080800; PIDN:AAD39310.1; GSPDB:GN

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394
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392 BTQPQSSPFSCMDLTY-VSLLLQEFGFP-RSKVLKLTRKI--DNVETSWALGAI-----
                                                                                                                               447
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 16, 2004, 16:34:13 ; Search time 196 Seconds (without alignments) 1338.627 Million cell updates/sec Run on:

US-09-905-589A-2 2364 1 MRKISNHGSLRVAKVAYPLG......ALGAIFHYIDSLNRQKSPAS 456 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O75354 homo canion		rattr		2	O8chz3 mus musculu	O6p6s9 rattus norv	Aah62044 rattus no	18 musco	mus	9 mu	mus	MILS	mus	862 mus	mus	mus	บพ ธนน		homo	mesoc	_	-	drosophila			_		ı u	Oganm7 dolichos bi	
SUMMARIES	ID	ENP6 HUMAN		ENP6 RAT	06YH <u>K</u> 4	AAN72326	Q8CHZ3	Q6P6S9	AAH62044	ENP5_MOUSE	Q8CD29	AAK82949	BAC29515	BAC29861	BAC37592	BAC37862	BAC38219	BAC40362	Q8BR23	ENPS HUMAN	Q96RX0	ENPS MESAU	Qecde	Q7PVI8	076268	09VQ18	Q9XU84	QGBUS6	GDA1 KLULA	08H7 <u>T</u> 6	O9SPM7	Q84UE0
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GDA1 SCHPO	Q84UD8	QBRVT6	Q9FUI1	O9SPM6	Q6CBK6	Q6FLR7	GDA1 YEAST	Q624 <u>P</u> 2	BAC83798	Q753F2	AAS53733	Q98QG2
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556	467	467	447	455	539	541	518	467	467	510	510	471
21.5	21.4	21.3	21.2	21.2	21.2	21.1	21.1	20.9	20.9	20.7	20.7	20.7
508	505.5	504.5	501,5	501	200	498.5	498	495	495	490	490	489.5
3.2	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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                                                                                                                                                                                A MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A pokins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
Diatchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A promatein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,
A Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Plakesley S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Pahak J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Raha A.C., Grimwood J., Schwuchenko Y., Bouffard G.G.,
A Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smallus D.E.,
A Chenzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBMEDITULAR LOCATION, AND TISSUE SPECIFICITY.

SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

PubMed=11041856; DOI=10.1021/bi0009592;

Yeung G., Mulero J.J., McGowan D.W., Bajwa S.S., Ford J.E.;

redominantly expressed in the heart.";

Biochemistry 39:12916-12923 (2000).

-!- FUNCTION: Might support glycosylation reactions in the Golgi apparatus and, when released from cells, might catalyze the hydrolysis of extracellular nucleotides. Hydrolyses preferentially nucleoside 5'-diphosphates are hydrolysed only to a minor extent, there is no hydrolysis of nucleoside 5'-monophosphates. The order of activity with different substrates is GDP > UDP = CDP >> ADP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                occurs in a soluble extracellular form.
TISSUE SPECIFICITY: Expressed in most tissues, but predominantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleotide + phosphate.
COFACTOR: Requires calcium and magnesium (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein. Golgi. But also
SEQUENCE FROM N.A., AND SOLUBLE FORM DISULFIDE BONDS.
PubMed=14529283; DOI=10.1021/bi035137r;
Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;
"Bacterial expression, characterization, and disulfide bond determination of soluble human NTPDase6 (CD39L2) nucleotidase: implications for structure and function.";
Biochemistry 42:11726-11735(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39 NTPASE; FALSE NEG.
Calcium, Glycoprotein; Golgī stack; Hydrolase; Magnesium;
Polymorphism; Signal-anchor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro; IPR000407; GDA1_CD39_NTPase.
Pfam; PF01150; GDA1_CD39; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY327581; AAP92131.1; -. EMBL; BC025980; AAH25980.1; -.
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MIM; 603160; -.
                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>LOASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 SFKGEWEHAEVIYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
                                                                                                                                                                                                                                                                                                                                                  29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            In soluble form.

In soluble form.

N-linked (GLONAC. .) (Potential).

N-linked (GLONAC. .) (Potential).

N-linked (GLONAC. .) (Potential).

/FIId=VAR_017863.
                                                                                                                                                                                                                                                                                             .,
                membrane
                                                                                                                                                                                                                                                          Length 484;
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GO, GO:0016787; F:bydrolase activity; IEA.
InterPro; IPR000407; GDAl_CD39_NTPase.
                                                                                                                                                                                                                                                                                               Indels
            Signal-anchor for type II protein (Potential). Lumenal (Potential).
                                                                                                                                                                   S -> N (in Ref. 3).
Missing (in Ref. 4).
E -> K (in Ref. 2).
604C958953179089 CRC64;
Cytoplasmic (Potential)
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Last annotation update)
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0
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Pred. No. 1.6e-177;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence upd
01-MAR-2004 (TrEMBLrel. 26, Last annotation u
Hypochhetical protein DKF2p761J1915 (Fragment)
Name-DKF2p761J1915;
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                                                                                                                                                                                                                                                              99.9%;
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484 AA;
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Matches
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us-09-905-589a-2.rup

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nucleotide + phosphate.
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                            LQASPEGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 347
                                                                                                                                                                                                                                                                                   SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 407
                                                                                                                                                                                                                                                                                                                        AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLOEFGFPRS 467
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                                                                                                                    SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
                                                                                                                               LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
                                                                                1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
                                                                                                                                                        VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
                                                                                                                                                                                             FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
                                                                                                                                                                                                               FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND CHARACTERIZATION STRAIN-Sprague-Dawley, TISSUE-Brain, MEDLINE-20498744; PubMed=11042118;
                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annocation update)
Ectonucleoside triphosphare diphosphohydrolase 6 (EC 3.6.1.6)
(NTPDase6) (CD39 antigen-like 2).
                                               Length 503;
                                                                 Indels
                           163933F9139D8D9F CRC64;
                                                                 ·.
                                                                                                                                                                                                                                                                                                                                              KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
                                            99.9%; Score 2361; DB 2;
99.8%; Pred. No. 1.7e-177;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                          455 AA
                          503 AA; 54763 MW;
Pfam; PF01150; GDA1 CD39;
                                                              455; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
       Hypothetical protein.
NON TER 1
SEQUENCE 503 AA; 5
                                                     Similarity
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                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRKIPNHGTLRMTKVAXPLGLCVGLFIYVAYIKWHRASAAQAFFIIAGAASGVRWTQQAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SSPDSATRGHEVFYGIMFDAGSTGTRIHVFQFARPPGETPTLTHETFKALKPGLSAYADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 FLVGDDCVSIMNGTDEGVSAWITVNFLTGSLKTPGSSSVGMLDLGGGSTQITFLPRVEGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
-!- COFACTOR: Requires calcium and magnesium.
-!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi. But also occurs in a soluble extracellular form.
-!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal-anchor for type II membrane protein (Potential).

Lumenal (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      In soluble form (By similarity).
In soluble form (By similarity).
N-linked (GlCNAc. .) (Potential)
N-linked (GlCNAc. .) (Potential)
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                                                                                                                                                                                                                                                                                                                    EMBL; AJ277748; CAC16598.1; -...
RGD; 619725; Entpd6.
InterPro; IPR00407; GDA1_CD39_NTPase.
Pro; IPR00150; GDA1_CD39_I.
PROS;TE; PS01239; GDA1_CD39_NTPASE; FALSE_NEG.
Calcium; Glycoprotein; Golgī stack; Hydrolase; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49899 MW; 19A22E8BAEF0F77B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Pred. No. 4.3e-154;
27; Mismatches 33;
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                                                                                                                                                                                                                                                  entities requires a license agreement (St
or send an email to license@isb-sib.ch).
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Matches 394; Conservative
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327
401
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Name=Entpd6;
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                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
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                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Bctonucleoside triphosphate diphosphohydrolase 6.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cavia
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TISSUE=Brain;
Mihaylova-Todorova S.T., Choe S.M., Miller L.J., Horowitz B.,
                                                                                                                                                                                                                        В.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 445;
                                                                                                                                                                                                  TISSUE-Brain;
Minaylova-Todorova S.T., Choe S.M., Miller L.J., Horowitz
Westfall D.D.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY149906; AAN72326.1; ---
EMBL; AX149906; AAN72326.1; ---
EMBL; PROGUEST, F.Hydrolase activity; IEA.
Interpro; IPR00407; GDAL_CD39.NTPase.
Pfam; PF01150; GDAL_CD39.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae,
                                                                                                                                                                                                                                                                                                                                                                                           445 AA; 48357 MW; 890CEFD068405698 CRC64;
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AAN72326;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   82.2%; Score 1943; DB 2;
82.9%; Pred. No. 1.4e-144;
iive 31; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 82.9
Matches 377; Conservative
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                                                                                                                                                                                  FROM N.A.
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                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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AAN72326
ID AAN72326
DT 02-M

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 IPVGSAAHALEVFYGIMFDAGSTGTRVHVFQFARPPGETPTLTHETFKALKPGLSAYADD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171
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                                                                                                                                                                                                                                                                                                                   1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
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MEDLINE-22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Dlatcherko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Blosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane B.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 VEKSAQGIQELLDVAKQDIPFDFWKATPLVLKATAGLKLLPGEKAQKLLQKVKEVFKASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
"Sequencing of an ectonucleoside triphosphate diphosphohydrolase homolog of NTPDase6 from guinea pig."; submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                         Length
                                                                                                                                          48357 MW; 890CEFD068405698 CRC64;
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1-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445
                                                                                                                                                                                                   82.2%; Score 1943; DB 2;
82.9%; Pred. No. 1.4e-144;
iive 31; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPA
                                                                                          EMBL; AY149906; AAN72326.1;
Hydrolase.
                                                                                                                                                                                                                                                                  Matches 377; Conservative
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                                                                                                                                                      445 AA;
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AAH62044;
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                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEKSAQGIQELLNVAKQHIPYDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
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                                                                                                                                                                                                                                                                                                                                                                                                               09
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                              1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAFGARWGQQAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buserow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                      52.0%; Score 1229.5; DB 2; Length 278; 85.6%; Pred. No. 1.4e-88; ive 17; Mismatches 18; Indels 5;
                                                                                                                                                                        Strausberg R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC038126; AH38126.1;
GO; MGI:1202295; Entpd6.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR000407; GDAl_CD39_NTPase.
PF01150; GDAl_CD39; 1.
                                                                                                                                                                                                                                                                                            75A92DD1AC76297F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 5.
Name=EBtpd5;
                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 AA
                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J, TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                            278 AA; 30130 MW;
                                                                                                   and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 237; Conserve
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                                                                                                                                                                                                                                                                                                             Query Mac.
                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                       Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 AAETHLIDYEKGGVLKVEDFERKAREVCDNLESFSSGSPFLCMDLSYITALLKDGFGFED 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Gener than 15,000 full-length human and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKBVFKASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 PKQGAETVQELLEVAKDSIPRSHWKRTPVVLKATAGLRLIPEQKAQTLLLEVEEIFKNSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.2%; Score 1021; DB 2; Length 4 53.2%; Pred. No. 6.9e-72; tive 58; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Prostate;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 AA; 47372 MW; 6CBBC44D96A60211 CRC64;
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                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC062044; AAHC044.1; -
EMBL; BC062044; AAHC044.1; -
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR00407; GDAI_CD39_NTPase.
Ffam; PF01150; GDAI_CD39; 1.
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02-MAR-2004 (TrEMBLrel. 27, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 53.2%
les 207; Conservative
                                                                                                                                                                                                                          and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                           TISSUE=Prostate;
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NTPases
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hashe F., Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.B., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Robar S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodrigues A.C., Grimwood J., Schuutz J., Myers R.M., Butterfield Y.S., Rzzwinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., J. Marra M.A.; Generation and initial analysis of more than 15,000 full-length human M. M. Madan A., Rodriguez D.M., Schein J.S., M. Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
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53.2%; Pred. No. 6.9e-72;
ive 58; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6CBBC44D96A60211 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Hydrolase.
                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 53.2%
---nes 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Prostate;
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O9WUZ9; 070214; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 05-UUL-2004 (Rel. 44, Last annotation update) Ectonucleoside triphosphate diphospholydrolase 5 precursor (EC 3.6.1.6) (WIPDase5) (Nucleoside diphosphatase) (CD39 antigen-like 4) (ER-UDPase).

OS CON CONTRACT OF THE CONTRAC

Name=Entpd5; Synonyms=Cd3914; Mus musculus (Mouse).

427 AA

STANDARD;

MOUSE ENPS\_MOUSE

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MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Butchow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Butchow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Schaetz T.E.,
Brownstein M.J., Widkin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,
A Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Willalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Tuuchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REP SUCDENCE FROM N.A.

REAGARAKY T. T.S.SUB-Kidney,

RA OKAZAKY Y. PUTUND M. KBAUKAWA T. Adachi J., BONO H., Kondo S.,

RA OKAZAKY Y. PUTUND M., KBAUKAWA T., Adachi J., BONO H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Schonbach C., Gojobori T.,

RA Jadarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schrim L.M., Kanapin A., Matcher C., Crothani L.E., Cousins S.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Blake J.A., Rawali T.A., Pletcher C.F., Forrest A., Frazer K.S.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Guydh J.,

RA Konajaya A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magshima T., Numata K., Okido T., Pavan W.J., Pertea G., Pescle G., Wang Y., Walls R., Schale R.D., Tromita M., Saltana R., Schneider C., Wang Y., Walls C., Wang Y., Walls C., Wang Y., Wallskawa T., Rounce K., Markawa T., Rounc M., Zavolan M., Zhu Y., Zimmer A., Arakawa T., Pekuda S., Ryanishi R., Yasaki J., Alakawa T., Rounc H., Nakamura M., Sakazume M., Sakai K., Rawai J., Alakawa Y., Shinagawa T., Rutuda S., Alarakhi A., Yashiraki T., Saraki K., Kawai J., Alakawa Y., Shinagawa T., Rounci H., Nakami H., Nakamura M., Sakai K., Sasaki Y., Sasaki W., Sanaki Y., Shinagawa T., Rounci H., Nakami Y., Shinagawa T., Rounci H., Nakami Y., Shinagawa T., Rounci H., Wangari H., Wallaki Y., Shinagawa T., Rounci H., Valaki Y.,
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Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trombetta E.S., Helenius A.; "Glycoprotein reglucosylation and nucleotide sugar utilization in the secretory pathway: identification of a nucleoside diphosphatase in the
                                                                                                                                                                                                                                                                                                  Chadwick B.P., Williamson J., Sheer D., Frischauf A.-M.; "CDNA cloning and chromosomal mapping of a mouse gene with homology to
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99298181; PubMed=10369669;
                                                                                                                                                                                                                                                               MEDLINE=98119025; PubMed=9457681;
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STRAIN=FVB/N; TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endoplasmic reticulum.";
EMBO J. 18:3282-3292(1999).
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                                                                                   NCBI_TaxID=10090;
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PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Entpd5;
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                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                           FUNCTION: Likely to promote reglycosylation reactions involved in glycoproteins folding and quality control in the endoplasmic reticulum. Hydrolyzes UDP, GDP and IDP but not any other nucleoside di-, mono- or triphosphates, nor thiamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLTAHKESEQHRDWLGLGGHLSPAPVSGHHQLRPSSTSEAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISEPVFSQEGVDSETFSDLSGKAWPETR (in Ref. 1)
2F9DA2C342C55577 CRC64;
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PROSITE; PS01238; GDA1_CD39 NTPASE; FALSE NEG.
Calcium; Endoplasmic reticulum; Glycoprotein; Hydrolase; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ^
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N-linked (GlcNAc. .) (Potential).
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DGTLLQLTKKVNNIETGWALGATFHLLQSLGITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                  pyrophosphate.
CATALYIC ACTIVITY: A nucleoside diphosphate + H(2)0 = a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 1007; DB 1; Length 427;
; Pred. No. 8.8e-71;
62; Mismatches 133; Indels 10
                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: Ubiquitous.
PTM: N-glycosylated; high-mannose type.
MISCELIANEOUS: Optimal pH is neutral.
SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ectonucleoside triphosphate diphosphohydrolase 5.
                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
                                                            Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                            COFACTOR: Requires calcium and magnesium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK002618; BAB22234.1; --
EMBL; BC015247; AAH15247.1; --
MGD; MG1:1321385; Enpgd..
InterPro; IPR000407; GDA1 CD39 NTPase.
Pfam; PF01150; GDA1 CD39; 1.
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                                                                                                                                                                                                       nucleotide + phosphate.
                                    and mouse cDNA sequences.
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Best Local Similarity 50.0
Matches 213; Conservative
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SIGNAL 18
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                                                            Proc. Natl.
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CONFLICT
CONFLICT
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298 GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYYDRAADTHLIDYEKGGVLKVEDFERK 357
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MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
                                                                            384 AKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIF
                                                                                                                              PERAIN-C57BL/64); PubMed=11076861; MEDLINE=20530913; PubMed=11076861; MEDLINE=20530913; PubMed=11076861; MEDLINE=20530913; PubMed=11076861; Medline T., Tashiro H., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., "RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2003 (TremBirel. 23, Last sequence update)
01-WAR-2004 (TremBirel. 26, Last annotation update)
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
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Genome Res. 10:1757-1771(2000)
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MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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MEDLINE=21085660; PubMed=11217851;
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STRAIN=C57BL/6J, TISSUE=Testis;
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MEDLINE=99437879; PubMed=10506756;
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           Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Harakida K., Hayatsu N., Hirawoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabb Y., Tagami M., Tagama A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001)
                                                                                                                                                                                                                                                                                                                                                                                          37 ATATQAFFSITRAAPGA-----RWGQ----QAHSPLGTAADGHEVFYGIMFDAGSTG
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                           ; Score 1007; DB 2; Length 427;
; Pred. No. 8.8e-71;
62; Mismatches 133; Indels 18
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Last annotation update)
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MGD; MGI:1321385; Entpd5.
GO; GO:0016787; F:hydrolase activity; IEA.
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Pfam; PF01150; GDA1_CD39; 1.
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    STRAIN=C57BL/6J; TISSUE=Testis;
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Mus musculus (Mouse).
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Les 213; Conservative
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SEQUENCE
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AC AAR82
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STRAIN=C57BL/6J; TISSUE=thymus;

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STRAIN=CS7BL/G87 IISSUE=Bone;
MADLINE=22354683; PubMed=12466851;
The FANTOM CONSOrtium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
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Vakaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
Recio J.A., Zambrano N., de La Pena L., Powers C., Siwarski D., Huppi K., Notario V.; "cDNA isolation, expression, and chromosomal localization of the
                                                                                                                                                                                                                18;
                                                                                                                                                                        Length 427;
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Adult male bone CDNA, RIKEN full-length enriched library,
clone:9830144N04 product:ectonucleoside triphosphate
diphosphohydrolase 5, full insert sequence.
                                                                                                                                                                                                                  Indels
                                                                   pcph proto-oncogene.";
Mol. Carcinog. 26:130-136(1999).
EMBL, AF136571; AAK82949.1; -
SEQUENCE 427 AA, 47101 MW; 2F9DA2C342C55577 CRC64;
                                                                                                                                                                      ch 42.6%; Score 1007; DB 2; 3 similarity 50.0%; Pred. No. 8.8e-71; 213; Conservative 62; Mismatches 133;
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STRAIN-C57BL/6J; TISSUE=Bone;
MEDLINE=21085660; PubMed=11217851;
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                                                                                     324 LHELCAARVSEVLONRVHRTEEVRHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383
                                                                                                                                 298 GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYYDRAADTHLIDYEKGGVLKVEDFERK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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                                                                                                                                                                                     384 AKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIF
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MEDLINE-20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Ritsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsunato H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wattahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mu
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
16 days neonate thywns cDNA, RIKEN full-length enriched library, clone:All30044A06 product:ectonucleoside triphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=22354683; PubMed=12466851;
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MEDLINE=21085660; PubMed=11217851;
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Adachi J., Aizawa T., Hanagaki T., Hirozane T.,
Hori F., Indcani K., Ishii Y., Itch M., Kagawa I., Ksukawa T.,
Adori F., Indcani K., Ishii Y., Itch M., Kagawa I., Ksukawa T.,
Akach H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Katch H., Kawai J., Kojima Y., Murata M., Oksato N.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A., Takakabahi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 of new genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/67, TISSUE-Bone;
MEDLINE-20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                   Shibata K., Itoh
                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Bone;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It
Konno H., Okazaki Y., Muramatsu M., Hayashizati Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                      Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                         STRAIN=C57BL/6J; TISSUE=Bone;
MEDLINE=99279253; PubMed=10349636;
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RIKEN FANTOM Consortium;
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                                                                                                SEQUENCE FROM N.A.
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STRAIN-C57BL/6J; TISSUB-Urinary bladder;
MEDLINE-20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                   the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; PubMed=11076861; STRAIN=C57BL/6J; PubMed=11076861; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Yamamoco R., Matsumoto H., Sakaguchi S., Ikegami T., Kashinagi K., Pujiwake S., Inoue K., Togawa M., Daraa B., Watshika M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RIKE integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequence:";
                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CS7BL/6J; TISSUB=Urinary bladder;
MEDLINE=9279233; PubMed=10349636;
Carninoi P., Hayashizahi Y.;
"High-efficiency full-length cDNA cloning.";
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                                                           STRAIN=C57BL/6J; TISSUB=Urinary bladder;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
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MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
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                                                                                                                                                                                            full-length cDNAs.";
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SEQUENCE FROM N.A.
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                                                                                                                      SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Thymus;
Adachi J., Aizawa K., Akimura;
Adachi J., Aizawa K., Akimura;
Adachi J., Aizawa K., Akimura;
A Hayashida K., Hangaki T., Hara A., Hashizume W.,
A Hori F., Innotani W., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Innotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Oksato H.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Adult male urinary bladder CDNA, RIKBN full-length enriched library,
clone:9530068A17 product:ectonucleoside triphosphate
diphosphohydrolase 5, full insert sequence.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771 (2000).
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiraoka T., Hiraoka T., Hirozane T., Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kowda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nokarawa T., Miyazaki A., Murata M., Nokarawi K., Sakai K., Sakazume M., Osatoh H., Sakai C., Sakai K., Sakazume M., Osatoh H., Sakai C., Sakai K., Sakazume M., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takaku-Akahira S., Takaku-Kahashi F., Takaku-Akahira S., Takaka W., Tanaka T., Johat J., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (ApR-2002) to the EMBL/GenBank/DDBJ databases.
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50.0%; Pred. No. 8.8e-71;
.ive 62; Mismatches 133; Indels
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TRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLDVAKQDIPFDF 143
                                                                                LHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383
                                                                                                                                                                                                                                                                       GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYXDRAADTHLIDYEKGGVLKVEDFERK 357
                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUB=Thymus;

MEDLINB=22354683; PubMed=12466851;

The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of

60,770 [ull-length cDNAs.";
                                                                                                                          INFLIGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMFNRTYKLYS
                                                                                                                                              STRAIN=C57BL/6J; TISSUB=Thymus;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                                                                       YSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQKAAAS
                                                                                                                                                                                                                    HSYLGFGLKAARLATLGALEAK-GTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEGEM
                                                            WKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
3 days neonate thymus cDNA, RIKEN full-length enriched library,
clone:A630007L13 product:ectonucleoside triphosphate
diphosphohydrolase 5, full insert sequence.
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MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length CDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSOTTIUM;
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Carraines Strong M. A. Akimura T., Arakawa T., Bono H., Carninci P., Rudda S., Purnon M., Hanagaki T., Hara A., Hashizume W., Puruda S., Purnon M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu M., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohasto N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Saito R., Shibata K., Shinagawa A., Shiraki T., Sogaba Y., Taqami M., A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
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                                                                                                                             STRAIN-C57BL/60; TISSUE-Thymus;
MEDLINE-20530913; PubMed=11076861;
MEDLINE-20530913; PubMed=11076861;
MEDLINE-20530913; PubMed=11076861;
Subitar K., Itoh M., Aizawa K., Naqsoka S., Sasaki N., Carninci P., Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rawai J., RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
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Search completed: November 16, 2004, 16:59:41

Job time : 201 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 16, 2004, 16:32:53 ; Search time 156 Seconds (without alignments) 1048.593 Million cell updates/sec

US-09-905-589A-2

Title:

2364 1 MRKISNHGSLRVAKVAYPLG......ALGAIFHYIDSLNRQKSPAS 456 Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2002273 seqs, 358729299 residues Searched:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Geneseq\_23Sep04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2000s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\*

SUMMARIES

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AAB72239	ADP07491	AAE19884	AD099448	AAB53336	ABB66213	ADQ99472	ABB59611	AAU30879	AAU30881	AAW85687	AAW85684	AAU78818	AAW85685	AAU78819	ADK36500	AD060417	ABP81286	ABM74049	ADJ57264
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405	407	465	465	330	461	461	464	141	144	467	462	462	486	486	139	455	472	457	454
38.5	38.5	38.2	38.2	34.8	26.3	26.3	26.3	25.2	25.2	21.9	21.4	21.4	21.2	21.2	20.9	20.7	20.7	20.6	20.5
606	606	904	904	823	621	621	621	596	296	518.5	206	206	501	501	495	490	488.5	486	485
26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

AAE19881 standard; protein; 456 AA. (first entry) 18-JUN-2002 AAE19881; RESULT 1 AAE19881 

Human CD39L2 protein.

Theumatoid arthritis, autoimmune thyroiditis, allergic reaction, asthmatis inheumatoid arthritis, autoimmune thyroiditis, allergic reaction, asthmatis inheumatoid arthritis, autoimmune thyroiditis, allergic reaction, asthmatis inspendent diabetes mellitus; periodontal disease; osteoporosis; osteoarthritis, wound healing; tiseare repair; Alzheimer's disease; parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease; nerve injury; ischaemia-reperfusion injury; nervous system disease; nerve injury; ischaemia-reperfusion injury; Crohn's disease; Crohn's disease; Crohn's disease; varucide; antibacterial; antifungal; neuroprotective; dermatological; immunosuppressive; vulnerary; nootropic; anticonvulsant; antiinflammatory; nephrotropic; gastrointestinal; vasotropic. Human; CD-39-like protein; CD39L2 protein; therapy; immune deficiency;

Homo sapiens

US6350447-B1.

26-FEB-2002.

99US-00240639. 29-JAN-1999; 99US-00240639. 29-JAN-1999;

(HYSE-) HYSEQ INC.

Chadwick BP, Frischauf A;

WPI; 2002-215262/27. N-PSDB; AAD31693 An isolated polypeptide with phosphohydrolase activity, designated CD39L2, useful to identify other proteins with which binding occurs or identify inhibitors and for treatment of, e.g., Alzheimer's, multiple sclerosis and osteoporosis.

Claim 1; Fig 4; 101pp; English.

The present invention relates to novel proteins with phosphohydrolase activity, designated CD-39-like (CD39L) proteins and polymucleotides

conditions such proteins. Last proteins are useful to thear infection that may diseases caused by viral, bacterial, fungal or other infection that may be treatable with CD39L. They are useful in the treatment of various immune deficiencies and disorders, autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune thyroiditis and insulin dependent diabetes mellitus, allergic reactions and conditions such as asthma and other respiratory problems, periodontal diseases, osteoporosis, osteoarthritis and other tooth repair processes. They may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration as well as for wound chealing and tissue repair and replacement and in the treatment of burns, inclsions and ulcers. CD30 proteins may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central nervous system diseases such as Alzheiner's disease, parkinson's disease, amyotrophic lateral sclerosis, Huntington's disease, peripheral nervous system diseases peripheral nervopathy and localised neuropathies. They are also used to treat mechanical and traumatic disorders which involve degeneration, cheating wounds including pressure ulcers which involve degeneration, cheating wounds, including pressure ulcers which involve degeneration, are also useful to promote better or faster closure of nonvascular insufficiency activity and may be used to treat inflammatory activity and may be used to treat inflammatory activity and may be used to treat inflammatory expectation or acute conditions), including present sequence is human CD39L2 protein VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240 SFKGEWEHAEVTYRVSGOKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300 LOASPPGYLTALRMENRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD **VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP** 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH CD39L proteins are useful to treat infectious 100.0%; Score 2364; DB 5; Length 456; 100.0%; Pred. No. 1.2e-215; ive 0; Mismatches 0; Indels 0 456 KVLKLTRKIDNVETSWALGAIFHYIDSLNROKSPAS Matches 456; Conservative such proteins. Best Local Similarity Sequence 456 AA; 361 421 301 61 61 121 121 181 181 241 301 Query Match g ŏ a ò \$ g g à qq 엄 ð ò ò

nuclectide triphosphatase, NTPase) and nucleic acid molecules encoding nucleited triphosphatase, NTPase) and nucleic acid molecules encoding such polypeptides. CD39-like polynucleotides may be used as hybridisation probes, PCR primers and in chromosome and gene mapping. Polypeptides of the invention may be used as molecular weight markers, as food supplements, in generating an antibody that specifically binds the polypeptide, as anti-thrombotic or anti-tissue graft rejection agents, or for regulating ATP neurotransmission in smooth muscle, peripheral ganglia or brain. Sequences of the invention are useful in modulating ecto-ATPase activity. The present sequence is human CD39-like protein, CD39L2. Note: This sequence is stated to be the same as that shown in Figures 8 and 9, however the sequence is truncated at it's N-terminal. The longer sequence is represented in ADQ99473. 121 VEKSAQGIRELLDVAKQDIPPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120 New CD-39-like polypeptides and polymucleotides, useful in chromosome and gene mapping, as molecular weight markers, as food supplements, or as anti-thrombotic or anti-tissue graft rejection agents. CD39-like protein; gene mapping; molecular weight marker; food supplement; anti-thrombotic; anti-tissue graft rejection agent; ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase; 1 MRKISNHGSLRVAKVAYPLGLCVGVF1YVAYIKWHRATATQAFFSITRAAPGARWGQQAH 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH The invention relates to novel CD39-like polypeptides (CD39-like 100.0%; Score 2364; DB 8; Length 456; 100.0%; Pred. No. 1.2e-215; ive 0; Mismatches 0; Indels 0; TII. "II ľΔI i. /note= "Apyrase region (ACR) /note= "Apyrase region (ACR) "Apyrase region region Claim 2; SEQ ID NO 2; 104pp; English cocation/Qualifiers 219. .239 /note= "Apyrase Human CD39-like protein, CD39L2 99US-00240639 13-JUL-2001; 2001US-00908510 Chadwick BP, Frischauf A; 23-SEP-2004 (first entry) Matches 456; Conservative .266 /note= NTPase; human; enzyme. WPI; 2004-515395/49. N-PSDB; ADQ99441. Local Similarity (NUVE-) NUVELO INC Sequence 456 AA; 29-JAN-1999; US6759214-B1. Homo sapiens 19 Query Match Region Region Region Region g à q ð à ö 120 9 9 0; KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456

09 9

ADQ99442 standard; protein; 456 AA

RESULT 2 ADQ99442

ADQ99442;

421

Gaps

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cerebral

arterial thrombosis,

cerebral ischaemia, angina,

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attery thrombosis or intracardiac thrombosis, and conditions associated with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in modulating disease states (including platelet aggregation, inflammation and apoptosis) associated with ADP or other purinergic signalling by reducing the levels of NDPs. The polypeptides are also useful for prophlaxis or treatment of inflammation related disorders, such as disorders involving sepsis or systemic inflammatory response syndrome or SIRS (and associated conditions such as fever, tachycardia, tachypnea, cytokine oversteinmlation), autoimmune disorders such as thrombosis, cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis; neurological disorders including neurodegenerative diseases, epilepsy, depression, Alzheimer's disease, Parkinson's disease, Huntington's sequence represents human CD39 like protein CD39-L2 err. The present

o,

Sequence 484 AA;

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240
                                                                                            241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGGVEGQPAKDGKELVSPCLSP 300
                                                                                                                     SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
                                                                                                                                        420
                                                                                                                                                                                    pathological
and
121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
                                                                                                                                                                                                                                                                                                                                                                                                    Human CD39-like protein, apyrase, NDPase, platelet function inhibitor, myocardial infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral artery thrombosis, platelet aggregation; inflammation, apoptosis, autoimmune disorder, neurological disorder;
                        FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQ1AFLPRVEGT
                                   LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
                                                                                                                                                                     AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotides encoding human CD39-like polypeptides, with apyrase and/or NDPase activity, which are useful in the treatment of pathol conditions caused by thrombosis (e.g. myocardial infarction) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's disease; Parkinson's disease; cancer; CD39-L2
                                                                                                                                                                                                                                                                                                                                                                              Human CD39 like protein CD39-L2 amino acid sequence.
                                                                                                                                                                                                                                   KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS
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11-JAN-2000; 2000US-00481238.
25-APR-2000; 2000US-00557800.
25-MAX-2000; 2000US-00583331.
30-JUN-2000; 2000US-00608285.
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ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase;
                                                                                29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAFGARWGQQAH
                                                                                                                                           89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
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                                                              1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
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                                  Gaps
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    Length 484;
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                                Indels
 ; Score 2364; DB 4;
; Pred. No. 1.3e-215;
0; Mismatches 0;
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100.0%;
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                               Matches 456; Conservative
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                  Local Similarity
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This invention relates to polynucleotides encoding human CD39-like polypeptides with apyrase and/or NDPase activity. The polypeptides having PTPDase, including NDPase, activity are useful for inhibiting platelet function and can therefore be used in the prophylaxis or treatment of pathological conditions caused by or involving thrombosis or excessive coagulation or excessive platelet aggregation, such as myocardial

Claim 39; Page 162-164; 203pp; English.

inflammatory disorders

ABB06124 standard; protein; 463 AA.

ABB06124

99US-00240639

Frischauf A;

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New CD-39-like polypeptides and polynucleotides, useful in chromosome and
                                                                                                               gene mapping, as molecular weight markers, as food supplements, or as anti-thrombotic or anti-tissue graft rejection agents.
                           13-JUL-2001; 2001US-00908510
                                                                                            N-PSDB; ADQ99441, ADQ99441.
                                                                                     WPI; 2004-515395/49.
                                                         (NUVE-) NUVELO INC
                                                                       Chadwick BP,
                                          29-JAN-1999;
US6759214-B1
              06-JUL-2004.
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ö nucleotide triphosphatase, Natacel and mucleic acid molecules encoding such polypeptides. CD39-11ke polynucleotides may be used as hybridisation probes, PCR primers and in chromosome and gene mapping. Polypeptides of the invention may be used as molecular weight markers, as food supplements, in generating an antibody that specifically binds the polypeptide, as anti-thrombotic or anti-tissue graft rejection agents, or for regulating ATP neurotransmission in smooth muscle, peripheral ganglia or brain. Sequences of the invention are useful in modulating ecto-ATPase activity and for identifying compounds that modulate ecto-ATPase activity. The present sequence is human CD39-11ke protein, CD39L2. Note: This sequence is stated to be the same as that shown in SEQ ID 2 of the sequence listing, however this sequence is longer at the N-terminal. The shorter sequence is represented in ADQ99442. SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKFGLSAYADD 120 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60 88 29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH Gaps The invention relates to novel CD39-like polypeptides (CD39-like . 0 Length 484; Indels 100.0%; Score 2364; DB 8; 100.0%; Pred. No. 1.3e-215; . 0; Mismatches Claim 2; Fig 8A-D; 104pp; English. Query Match Best Local Similarity 100. Matches 456; Conservative Sequence 484 AA; 61

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Human; cytostatic; osteopathic; gynaecological; neuroprotective;

W antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;

KW antiarteriosolerotic, antiplanmatory; dermatological;

KW antiarteriosolerotic; antiarthritic; antiarcoagulant;

KW antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;

KW anticonvulsant; antialabetic; tranquilliser; antidepressant; aeuroleptic;

KW anticonvulsant; antialabetic; tranquilliser; antidepressant; aeuroleptic;

KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;

KW contraceptive; degenerative disease; multiple solerosis; psoriasis;

KW rheumation; skin disease; multiple solerosis; glaucoma;

KW inflammation; skin disease; coagulation disease; habstrainty; cardiovascular disease; coagulation disease; bypertension;

KW inflammation; skin disease; epilepsy; angina; neurodegeneration;

KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;

KW gastric ulcer; Alzheimer's disease. Human NS protein sequence SEQ ID NO:216. (first entry) 10-MAY-2002 

Homo sapiens

24-JAN-2002

17-JUL-2001; 2001WO-IL000653 18-JUL-2000; 2000IL-00137345 15-DEC-2000; 2000IL-00140354

(COMP-) COMPUGEN LTD

Bernstein J; Mintz L, Freilich S,

WPI; 2002-155037/20. N-PSDB; ABL39778

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One hundred and twenty eight novel nucleic acid sequences, useful for treating and diagnosing e.g. cancer, asthma and Alzheimer's.

Claim 6; Page 251-253; 290pp; English

ABL39691 to ABL39818 represent novel human nucleic acid sequences encoding the proteins given in ABB06037 to ABB06164. The novel sequences (MS) can have cytostatic, osteopathic, gynaecological, neuroprotective, antiarthritic, antiposciatic, ophthalmological, virucide, vasotropic, antiarthritic, antiaflammatory, dermatological, virucide, vasotropic, antiarteriosclerotic, antiinflammatory, dermatological, anorecide, manulatt, anti-HIV, antiinflammatory, dermatological, anticogoulatt, antifibrinolytic, hypotension, antiasthmatic, cardiovascular, antidoperssant, gastroinfestinal, auroloptic, tranquilliser, antiulcer, antidopersessant, gastroinfestinal, auroloptic, crebroprotective, nootropic and contraceptive activities. The NS can be used in vaccines, contropical and contraceptive activities. The NS can be used in vaccines, dentifodies from the present invention can be used for treating and citagnosing e.g. cancer, osteoporosis, endometriosis, degenerative diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis, diseases, dystonia, multiple sclerosis, inflammation, skin disorders, disease, colepty, muscular dystrophy, AlDS, infertility, cardiovascular disease, colepty, muscular dystrophy, AlDS, infertility, cardiovascular disease, epilepsy, angina, neuroadegeneration, diabetes, anxiety, depression, schizophrenia, viral disease, gastric ulcers, stroke, alzeniemer's disease and as a contraceptive

Sequence 463 AA;

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                                                                                                           SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPCLSAYADD 120
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                                                                                                                                                                                                                                           FLVGDDCVSIMNGTDEGVSAMITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLFRVEGT 247
                                                                                                                                                                                                                                                                           LOASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
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                                                                                                                                                                VEKSAQGIRELLDVAKQDI PFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKBVFKASP
                                                      1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
                                                                             8 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
                                                                                                                          128 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
                                                                                                                                                                                                                    FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGT
                                  Gaps
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       Length 463;
                               0; Indels
99.9%; Score 2361; DB 5;
99.8%; Pred. No. 2.3e-215;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
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              Similarity
Query Match
Best Local S:
Matches 455
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ABJ04657 RESULT

ABJ04657 standard; protein; 467

(first entry) 11-OCT-2002

ABJ04657;

Protein of NOVX 15a SEQ ID No 36.

Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antilipaemic; neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective; tranquiliser; neuroleptic; antidabetic; antidabetic; antidiabetic; antidabetic; disorder; description metabolic syndrome X; wasting disorder; dancer; neurological disorder; esplepsy; stroke; mental disorder; schizophrenic disorder; vesicular transport; cystic fibrosis; gastrointestinal disorder; diabetes mellitus; ulcerative colitis; AIDS; allergic reaction; multiple sclerosis; rheumatoid arthritis; transgenic animal; gene therapy

Unidentified

06-DEC-2001; 2001WO-US046586

06-DEC-2000; 2000US-0251660P. 12-DEC-2000; 2000US-0255029P. 08-JAN-2001; 2001US-0260326P. 

2001US-0269942P. 2001US-0286183P. 2001US-0313627P. 2001US-0318712P. 24-JAN-2001; 2 20-FEB-2001; 2 24-APR-2001; 2 12-SEP-2001; 20-AUG-2001; 

(CURA-) CURAGEN CORP

i, Patturajan M, Shimkets RA, Casman SJ, Malyankar UM; Vernet CAM, Spytek KA, Shenoy SG, Alsobrook JP; Peyman JA, Stone DJ, Ellerman K, Gangolli EA, Boldog FlEisen AJ, Liu X, Padigaru M, Spaderna SK, Zerhusen BD; Guo X, Li L, Patturajan Tchernev VT, Vernet CAM, Colman SD, Eisen AJ, Edinger S,

WPI; 2002-547774/58. N-PSDB; ABT05470, Novel isolated polypeptide, designated NOVX, useful for treating opreventing cancer, diabetes, obesity, dyslipidemia, anorexia, and metabolic, neurodegenerative, immune and hematopoietic disorders.

Claim 1; Page 140; 421pp; English.

The invention relates to an isolated polypeptide, designated NoVX, comprising a sequence fully defined in the specification. The isolated protein, its encoding polymuclectide or an antibody created from the protein is useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NoVX-associated disorder, or for treating or preventing a NOVX-associated disorder in a subject, preferably muman. The isolated protein, its encoding polymuclectide or an antibody created from the protein are also useful for treating or preventing metabolic disorders, diabetes, obesity, infectious disease, ancorexia, neurodegenerative disorder, Alaheimer's disorders, and various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X, wasting disorders associated with obesity, the metabolic syndrome X, wasting disorders associated with objunclectide or an antibody created from the protein are useful for treating or preventing neurological disorders such as epilepsy, stroke, disorders including mood, anxiety, schizophrenic disorders.

C mental disorders including mood, anxiety, schizophrenic disorders, mellitus, goiter, gastrointestinal disorders including ulcerative colitis, other conditions associated with abnormal vesicle trafficking c including AIDS, allergic reactions, multiple sclerosis and rheumatorid arther atting or prevention who wenter of the invention is useful for artherial and and any or the invention is useful for arthritis. A cell comprising the vector of the invention is useful for producing non-human transgenic animals. The polynucleotide of the invention can be used to treat disorders by gene therapy. This sequence represents one of the isolated NOVX proteins of the invention

Sequence 467 AA;

0 9 71 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 12 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH Gaps . 0 Length 467; Indels 99.9%; Score 2361; DB 5; 99.8%; Pred. No. 2.4e-215; ive 1; Mismatches 0; Query Match Best Local Similarity 99.8 Matches 455; Conservative

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121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180 240 191 181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT à d ò

251 300 241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 192 FLVGDDCVSIMNGTDEGVSAMITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT ð

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SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primers useful for synthesizing full length cDNA clones and their use
                                                             420
        360
                        312 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLONRVHRTEEVKHVDFYAFSYYYDL
                                                                             AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
        SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL
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T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID NO 4100; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ishii S, I
S, Otsuki
                                                                                                                                                                                                                                                                                                                         Human; full length cDNA; cDNA synthesis; oligo-capping
                                                                                                                   KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
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Pred. No. 2e-214;
1; Mismatches 2;
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K, Kojima S,
                                                                                                                                                                                                                 AAM93929 standard; protein; 456 AA
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su A, Sugiyama T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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Best Local Similarity 99.3°
---nhes 453; Conservative
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N-PSDB; AAK94892.
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                                                                                                                                                                                                                                                                                                                                                                                 EP1130094-A2
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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/target molecules in the field of medicine, and in particular genes
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61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADD 120
                                       VEKSAQGIRELLDVAKQDI PFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
                                                                 121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATVGLRLLPGEKAQKLLQKVKEVFKASP
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                                                                                                                                                                                                                                              361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
                                                                                                    FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
                                                                                                                    SPKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; medicine; signal transduction; glycoprotein; transcription; oligo-capping method.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein encoded by a full length cDNA clone SegID 4100.
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Nagai K, Kojima S, Otsuki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                KVLKLTRKIDNVETSWALGAIFHYIDSLNROKSPAS 456
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02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
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N-PSDB; ADL32066.
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1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATAIQAFFSITRAAPGARWGQQAH

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encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polypeptide sequence is a full length human protein of the invention.
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                                                                                                                                                                                                                                1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATAIQAFFSITRAAPGARWGQQAH
                                                                                                                                                                                                                                                                      61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
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   8X88888
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      ADC14220 standard; protein; 450
                   (first entry)
                          Human enzyme ENZM-26.
                   18-DEC-2003
            ADC14220;
   ADC14220
RESULT
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FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGT FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 59 19 89 121 149 181 q 셤 à g a à ð à enzyme; human; ENZM; cytostatic; antiarteriosclerotic; antidiabetic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiaileragic; antiinflammatory; thyromimetic; gene therapy; cell proliferative disorder; endocrine disorder; neurological disorder; immune system disorder; inflammatory disorder; developmental disorder; reproductive disorder; vesicle-trafficking disorder; infection. 28-SEP-2001; 2001US-0326388P. 12-OCT-2001; 2001US-0328979P. 19-OCT-2001; 2001US-0346034P. 26-SEP-2002; 2002WO-US031096 WO2003042357-A2 sapiens 22-MAY-2003

Homor

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The invention relates to a novel isolated human enzyme (ENZM)

polypeptide. A polypeptide of the invention has cytostatic,
antiatrerioscalerotic, antidabetic, anticonvulsant, nootropic,
nutriarterioscalerotic, antidabetic, and thyromimelic activity. A polynucleotide encoding a polypeptides and polynucleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased

expression or overexpression of ENZM, such as cell proliferative (e.g. cancer, atherosclerosis), andoorine (e.g. diabetes), neurological (e.g. epilepsy, Huntington's disease, stroke), immuned, inflammatory (e.g. AIDS, allergies), developmental (e.g. Hypothyroidism, Cushing's syndrome), reproductive and vesicle-trafficking disorders, or infections. These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of ENZM. The ENZM or its fragments are useful in screening compounds for effectiveness as as agonist or antagonist of the polypeptides, or in altering the expression of modulate the activity of the polypeptide, The microarity is useful in monitoring and mino acid sequences of ansetul in monitoring and mino acid sequences of modulate the activity of the polypeptide. The microarity is useful in monitoring and antiput interpretable in monitoring and antiput interpretable and antiput inte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human enzymes (ENZM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant ENZM expression e.g.
                                                                                                                                                                                                                                                                                                                                                              Baughn MR;
                                                                                                                                                                                                                                                                                                                         Yang J, Lu DAM, Yue H, Elliott VS, Warren BA, Duggan BM;
Forsythe IJ, Lee EA, Hafalia AJA, Ramkumar J, Chawla NK, Baughn MR
Becha SD, Gorvad AB, Tran UK, Li JX, Yao MG, Ison CH, Griffin JA,
Lee SY, Chang H, Emerling BM, Tang YT, Lal PG, Kable AE;
Marquis JP, Jiang X, Jackson AA, Zebarjadian Y, Swarnakar A;
Wilson AD, Jin P, Richardson TW, Bhatia U, Burrill JD, Lee S;
Blake JJ, Ho A, Zheng W, Gao J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGOOAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monitoring or measuring protein-protein interactions, drug-target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interactions, and gene expression profiles. The sequences shown ADC14195-ADC14247 represent ENZM proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.0%; Score 2152; DB 7;
92.3%; Pred. No. 1.7e-195;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer, diabetes, epilepsy, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 26; 416pp; English.
                         2001US-0338048P.
2001US-0332340P.
2001US-0369725P.
2002US-0368799P.
2002US-0381558P.
2002US-0381558P.
                                                                                                                                                                                                                                                                            (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 421; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-449567/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADC14273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 450 AA;
26-OCT-2001;
08-NOV-2001;
16-NOV-2001;
                                                                                                      29-MAR-2002;
29-MAR-2002;
17-MAY-2002;
07-JUN-2002;
21-JUN-2002;
                                                                                  14-DEC-2001;
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240

184

-----YADD 124

88

Gaps

26;

Length 462; Indels

Score 2135; DB 4; Pred, No. 7.5e-194;

2; Mismatches

300

244

AAU30882

a à

g  $\delta$ Q ò 304

360

418

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neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective; randiparkinsonian; anticonvulsant; cerebroprotective; randipartic antidabetic; antidate; antidates; antidates; antidates; antiallers; antiallers; antiallers; antiallers; antiallers; antiallers; antiallers; antiallers; antidates; metabolic disorder; obssity, infectious disease; Alzheimer's disease; anorexia, neurodegenerative disorder; Parkinson's disorder; obssity; immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease; metabolic syndrome X; wasting disorder; cancer; neurological disorder; epilepsy; stroke; mental disorder; schizophrenic disorder; diabetes mellitus; ulcerative colitis; AlDS; allergic reaction; multiple sclerosis; rheumatoid arthritis; transgenic animal;
                                                                                                                                                                                                                                                                                                                  VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 364
                                                                                                                                                                                                         SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 AAGVGLIDAEKGGSLVVGDFEIAAKYVCVRTLGETQPQSSPFSCMDLTYVSLLLQEFGFP 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antilipaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 LQASPPRYLTALRMFNRTYKLYCYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
                                                                                                                                                           MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRANATQAFFSITRAAPGARWGQQAH
                                                                                                                                                                                                                                                                                                                                                             125 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                FLYGDDCVSIMNGTNEGVSAWITINFLTGSLKTPRRSNVGMLDLGGGSTQIVFLTHVEGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL
                                                                                                                                                                                                                                                                                                                                                                                                                        FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 AAGVGLIDAEKGGSLVVGDFEIAAKYVC-RTL-ETQPQSSPFSCMDLTYVSLLLQEFGFP
                                                                                                        1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 RSKVLKLTRKIDNVETSWALGAIFHYIDSLNROKSPAS 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425 RSKVLKLTRKIDNVETSWALGAIFHYIDSLNROKSPAS 462
                                                                                                                                                                                                                                                                  SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein of NOVX 15b SEQ ID No 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABJ04658 standard; protein; 446
90.3%;
92.1%;
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        Query Match 90.3'
Best Local Similarity 92.1'
Matches 422, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy
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                                                                                                                                                                                                                    361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
                                                                                                                                                                                                                                                               AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 414
             LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
                                                                                                                                              Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, vaccination, gene therapy, nutritional supplement,
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression; immune stimulation, anti-inflammatory; leukaemia.
                                           KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
                                                                                                                                                                                                                                                                                                                                                                KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 365; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human secreted protein #1373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΑĄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU30882 standard; protein; 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-2001; 2001WO-US008656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200179449-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2001
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                                                                                                                                                                                                                                                                                                                             421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU30882;
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                                                                                                                                                                                                                                                                          355
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06-DEC-2000; 2000US-0251660P. 12-DEC-2000; 2000US-0255029P. 08-JAN-2001; 2001US-0260326P.

Sequence 462 AA;

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The invention relates to an isolated polypeptide, designated NoVX, comprising a sequence fully defined in the specification. The isolated protein is useful in the manufacture of a medicament for treating a protein is useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NoVX-associated disorder, or for treating or preventing a NOVX-associated disorder in a subject, preferably human. The isolated protein its encoding cubject, preferably human. The isolated from the protein are also useful confortations disease, an antibody created from the protein are also useful confortations disease, anorexia, neurodegenerative disorder, Albahamer's disease, parkinson's disorder, immune disorders, disease, parkinson's disorder, immune disorders, diseases, and various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X, wasting disorders associated with obscity, the metabolic syndrome X, wasting disorders associated with chronic diseases, and cancer. The isolated protein are useful for treating or preventing neurological disorders such as epilepsy, stroke, creating or preventing metabolic syndrome X chizophrenic disorders.

CC treating or preventing metabolic such as cystic fibrosis, diabetes constitutes, goiter, gastrointestinal disorders including ulcerative colities, other conditions associated with abnormal vesicle trafficking including AIDS, allergic reactions, multiple sclerosis and rheumatoid contucing non-human transgenic animals. The polynucleotide of the producing non-human transgenic animals. The polynucleotide of the invention can be used to treat disorders by gene therapy. This sequence treat services and content of the invention so the termine content is carefully and the sequence of the isolated NoVX proteins of the invention
                                                                                                                                                                                                 Guo X, Li L, Patturajan M, Shimkets RA, Casman SJ, Malyankar UM; Tchernev VT, Vernet CAM, Spytek KA, Shenoy SG, Alsobrook JP; Edinger S, Peyman JA, Stone DJ, Ellerman K, Gangolli EA, Boldog Fl Colman SD, Eisen AJ, Liu X, Padigaru M, Spaderna SK, Zerhusen BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated polypeptide, designated NOVX, useful for treating preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and metabolic, neurodegenerative, immune and hematopoietic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 141; 421pp; English.
                        20-FEB-2001; 2001US-0269942P.
24-APR-2001; 2001US-02861B3P.
20-AUG-2001; 2001US-0313627P.
2001US-0263800P
                                                                                                   2001US-0318712P
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                                                                                                                                                   (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                  WPI; 2002-547774/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 415; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 446 AA;
                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABT05471
                                                                                                   12-SEP-2001;
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38; Gaps 89.5%; Score 2116; DB 5; Length 446; 91.0%; Pred. No. 4.6e-192; 2; Indels

SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120 29 MRKI SNHGSLRVÁV-----ARWGQQAH 50 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP

LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300 231 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKGVFKASP FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 171 181

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410 351 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTVVSLLLQEFGFPRS SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 291 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTBEVKHVDFYAFSYYYDL 421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456 411 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 446 g Pb d 8 ð

AAB72242 standard; protein; 471

AAB72242;

14-MAY-2001 (first entry)

Mature human CD39 like protein CD39-L2 amino acid sequence.

thrombosis; Human CD39-like protein; apyrase; NDPase; platelet function inhibitor; myocardial infarction, cerebral ischaemia, angina, arterial threcerebral artery thrombosis, platelet aggregation, inflammation, apoptosis, autoimmune disorder, neurological disorder, Alzheimer's disease; Parkinson's disease; cancer; CD39-L2.

Homo sapiens

WO200110205-A1.

15-FEB-2001

09-AUG-2000; 2000WO-US021790.

2000US-00481238. 2000US-00557800. 2000US-00583231. 2000US-00608285. 99US-00370265. 09-AUG-1999; 11-JAN-2000; 25-APR-2000; 26-MAY-2000; 30-JUN-2000; 

(HYSE-) HYSEQ INC.

Yeung G; Mulero JJ, Ford J,

WPI; 2001-147489/15 N-PSDB; AAF63387 Polynucleotides encoding human CD39-like polypeptides, with apyrase and/or NDPase activity, which are useful in the treatment of pathological conditions caused by thrombosis (e.g. myocardial infarction) and inflammatory disorders.

Claim 53; Page 192-194; 203pp; English.

This invention relates to polynucleotides encoding human CD39-like polypeptides with apyrase and/or NDPase activity. The polypeptides having prolypeptides with apyrase and/or NDPase activity. The polypeptides having ATPDAse, including NDPase, activity are useful for inhibiting platelet function and can therefore be used in the prophylaxis or treatment of pathological conditions caused by or involving thrombosis or excessive coagulation or excessive platelet aggregation, such as myocardial infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral artery thrombosis or intracardiac thrombosis, and conditions associated with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in modulating disease states (including platelet aggregation, inflammation and apoptosis) associated with ADP or other purinergic signalling by reducing the levels of NDPs. The polypeptides are also useful for prophylaxis or treatment of inflammation related disorders, such as prophylaxis or treatment of inflammation related disorders; such as classification or systemic inflammatory response syndrome or SIRS (and associated conditions such as fever, tachycardia, tachypnea,

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                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD39-L4; human; apyrase; nucleotide diphosphatase; NDPase; ATP Diphosphohydrolase; ATPDase; adenosine diphosphate; ADP; treatment; platelet aggregation; antithrombotic; thrombosis; myocardial infarction; cerebral isolatenia; angina; vascular graft; extracorporeal circulation; molecular weight marker; nutritional supplement; tumour; prevention; drug targeting; Apyrase Conserved Region; ACR.
                 atherosclerosis, acute pancreatitis, dermatitis, including psoriasis, cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis; neurological disorders including neurodegenerative diseases, epilepsy, depression, Alzheimer's disease, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis; and cancer. The present sequence represents mature D39 like protein CD39-L2
                                                                                                                                                                                                                                                                                           1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
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overstimulation); autoimmune disorders such as thrombosis
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/note= "Homologous to human and murin
                                                                                                                                                                                               Score 2003; DB 4; I
Pred. No. 2.8e-181;
1: Mismatches 5;
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/label= Leader_peptide
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The present amino acid sequence is the CD39-L4 protein, an apyrase and/or nucleotide diphosphatase (NDPase). It is isolated from the human foetal liver-splean cDNA library, b2HFLS20W. It is a soluble ATP Diphosphohydrolases (ATPDase) and is involved in the hydrolysis of adenosine diphosphate (ADP), the agonist that causes platelet aggregation. CD39-L4 protein has 30% and 80% homology to human and murine CD39-L4 is used to treat or prevent thrombosis, myocardial infarction, cerebral ischaemia and angina. It is also used in vitro, to maintain vascular grafts or during extracorporeal circulation, to hydrolyse NDP, as molecular weight markers and as nutritional supplements. It is used to adentify therapeutic agents that bind and modulate CD39-L4. It is coupled to toxins for targeting drugs to tumours or other cells that express CD39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid encoding human CD39-like protein, useful for treating preventing thrombotic disease.
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                        199. .206
/note= "Conserved motif in ATPDases"
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52.4%; Pred. No. 8.6e-86;
ive 56; Mismatches 123;
/label= Apyrase_Conserved_Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Fig 2; 125pp; English
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98US-00122449.
99US-00244444.
99US-00273447.
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Matches 204, Conservative
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04-FEB-1999;
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180 156 240 216

96

300

275

420 SKVLKLTRKIDNVETSWALGAIFHYIDSL

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Human CD39-like protein, apyrase, NDPase, platelet function inhibitor, myocardial infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral artery thrombosis, platelet aggregation; inflammation, apoptosis, autoimmune disorder, neurological disorder, all abanes, Parkinson's disease, cancer, CD39-L4.
                                                                                               Human CD39 like protein CD39-L4 amino acid sequence.
396 STVLOLTKKVNNIETGWALGATFHLLOSL 424
                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Fig 2; 203pp; English.
                                               AAB72238 standard; protein; 428
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                                                                                                                                                                                                                                          2000US-00481238.
2000US-00557800.
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                                                                                                                                                                                                                                   99US-00370265
                                                                                                                                                                                                                                                          26-MAY-2000; 2000US-00583231,
30-JUN-2000; 2000US-00608285,
                                                                                                                                                                                                                                                                                                     Yeung
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                    Mulero JJ,
                                                                                                                                                                                                                                                                                                                   WPI; 2001-147489/15.
                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                              N-PSDB; AAF63383.
                                                                                                                                                                                WO200110205-A1.
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25-APR-2000;
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                  09-AUG-1999;
                                                                                14-MAY-2001
                                                                                                                                                                                                  15-FEB-2001
                                                               AAB72238
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                                       AAB72238
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Polynucleotides encoding human CD39-like polypeptides, with apyrase and/or NDPase activity, which are useful in the treatment of pathological conditions caused by thrombosis (e.g. myocardial infarction) and

This invention relates to polynuclectides encoding human CD39-like
polypeptides with apyrase and/or NDPase activity. The polypeptides having
ATPDASS, including NDPase, activity are useful for inhibiting platelet
function and can therefore be used in the prophylaxis or treatment of
cagulation or excessive platelet aggregation, such as myocardial
infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
cartery thrombosis or intracardiac thrombosis, and conditions associated
with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
caulating disease states (including platelet aggregation, inflammation
condulating the levels of NDPs. The polypeptides are also useful for
cand apoptosis) associated with ADP or other purinergic signalling by
cc reducing the levels of NDPs. The polypeptides are also useful for
cptophylaxis or treatment of inflammation related disorders, such as
disorders involving sepsis or systemic inflammatory response syndrome or
cytokine overstimulation); autoimmune disorders such as thrombosis,
contrabosis, respectusion injury, asthma, multiple sclerosis, arthritis;
c neurological disorders including neurodegenerative diseases, epilepsy,
depression, Alzheimer's disease, parkinson's diseases, Huntington's
contractor entered by a such as a contactor entered by a contactor entered by a contactor entered contactor entered contactor entered contactors en sequence represents human CD39 like protein CD39-L4

Sequence 428 AA;

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                                                                                                                                                                                                     96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myocardial infarction; cerebral ischaemia; angina; arterial thrombosis; cerebral artery thrombosis; platelet aggregation; inflammation; apoptosis; autoimmune disorder; neurological disorder; Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
                                                                                                                                   PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD
                                                                                                                                                                              40 PINVSA----STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILLEGEVFDSVKPGLSAFVDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR
                                                                                                                                                                                                                                                                121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
                                                                                                                                                                                                                                                                                                                           97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP
                                                                                                                                                                                                                                                                                                                                                                                          FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
                                                                              Gaps
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                Length 428
                                                                           Indels
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         ; Score 999; DB 4; L, Pred. No. 8.6e-86; 56; Mismatches 123;
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             42.3%;
52.4%;
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25-APR-2000; 2000US-00557800.
26-MAY-2000; 2000US-00583231.
30-JUN-2000; 2000US-00608285.
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Query Match
Best Local Similarity 52.4*
Matches 204; Conservative
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conditions caused by thrombosis (e.g. myocardial infarction) and
                                                inflammatory disorders.
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9; Page 142-144; 203pp; English

This invention relates to polymucleotides encoding human CD39-like

polypeptides with apyrase and/or NDPase activity. The polypeptides having

the APPDase, including NDPase, activity are useful for inhibiting platelet

tunction and can therefore be used in the prophylaxis or treatment of

tunction and can therefore be used in the prophylaxis or treatment of

coagulation or excessive platelet aggregation, such as myocardial

infarction, cerebral ischaemia, angina, arterial thrombosis or excessive

coagulation or excessive platelet aggregation, such as myocardial

artery thrombosis or intracardia chrombosis, and conditions associated

with venous thrombosis. CD39-14 and CD39-12 polypeptides are useful in

modulating disease states (including platelet aggregation, inflammation

complying associated with ADP or other purinergic signalling by

reducing the levels of NDPs. The polypeptides are also useful for

complying sepsis or systemic inflammatory response syndrome or

SIRS (and associated conditions such as fever, tachycardia, tachypnea,

cyckokine overstimulation); autoimmune disorders such as thrombosis,

cytokine overstimulation); autoimmune disorders such as thrombosis,

cherrosis, reperfusion injury, asthma, multiple sclerosis, arthritis;

cherrological disorders including neurodegenerative diseases, epilepsy,

disease, and amyotrophic lateral sclerosis, and cancer. The present

cycknown and anyotrophic lateral sclerosis, and cancer. The present 

Sequence 428 AA;

62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120 121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGIRLLPGEKAQKILQKVKEVFKASP 180 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96 6; Gaps Length 428; Query Match 42.3%; Score 999; DB 4; Length 42 Best Local Similarity 52.4%; Pred. No. 8.6e-86; Matches 204; Conservative 56; Mismatches 123; Indels 40 g g ò

241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 157

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301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360  AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419 361

SKVLKLTRKIDNVETSWALGAIFHYIDSL 448 STVLQLTKKVNNIETGWALGATFHLLOSL 424 420

Search completed: November 16, 2004, 16:56:11 Job time : 160 secs

us-09-905-589a-2.rapb

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
               Copyright
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(without alignments) 1136.208 Million cell updates/sec November 16, 2004, 16:59:49 ; Search time 142 Seconds - protein search, using sw model OM protein Run on:

Title: Perfect score:

1 MRKISNHGSLRVAKVAYPLG......ALGAIFHYIDSLNRQKSPAS 456 US-09-905-589A-2 2364 Seguence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Total number of hits satisfying chosen parameters:

1568699 seqs, 353819137 residues

Searched:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:\*

1: cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:\*

2: cgn2-6/ptodata/1/pubpaa/US07 PUBCOMB.pep:\*

3: cgn2-6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

4: cgn2-6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: cgn2-6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

7: cgn2-6/ptodata/1/pubpaa/US08\_WBW PUB.pep:\*

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8: cgn2-6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

10: cgn2-6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

10: cgn2-6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

11: cgn2-6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

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14: cgn2-6/ptodata/1/pubpaa/US00\_PUBCOMB.pep:\*

15: cgn2-6/ptodata/1/pubpaa/US00\_PUBCOMB.pep:\*

16: cgn2-6/ptodata/1/pubpaa/US100\_PUBCOMB.pep:\*

17: cgn2-6/ptodata/1/pubpaa/US100\_PUBCOMB.pep:\*

18: cgn2-6/ptodata/1/pubpaa/US10PUBCOMB.pep:\*

19: cgn2-6/ptodata/1/pubpaa/US10PUBCOMB.pep:\*

19: cgn2-6/ptodata/1/pubpaa/US10PUBCOMB.pep:\*

10: cgn2-6/ptodata/1/pubpaa/US10PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### Sequence 27, Appl Sequence 123, Appl Sequence 124, Appl Sequence 124, Appl Sequence 125, Appl Sequence 271, Appl Sequence 271, Appl Sequence 125, Appl Sequence 125, Appl Sequence 27, Description Sequence Sequence Sequence US-10-286-926-27 US-10-211-913-123 US-10-211-913-136 US-10-211-913-134 US-10-211-913-134 US-10-211-913-125 US-10-211-913-271 US-10-091-085-3 US-10-091-085-5 US-10-092-063-3 US-10-092-063-5 SUMMARIES Query Match Length 1000.0 1000.0 1000.0 999.9 899.7 887.3 882.7 4 4 2 2 .6 4 2 2 .3 4 2 2 .3 2364 2364 2364 2361 2357 2116 2063.5 1954 1007 Score Result

Semience 3. Appli			Segmence 7. Appli				Semience 25, April	Segmence 25. Appl	Semience 39. April	Sequence 876, App	Sequence 876, App	Seguence 6447. An	Segmence 19. Appl	Seguence 36762. A	Segmence 2169. An	Semience 2. Appli	Semience 45875 A	Semience 9. Appli	Semience 334050	Segrence 230158	Segmence 1713. An	Seguence 132351	Secuence 49933. A	Sequence 185050.	Sequence 51762. A	Sequence 145076.	Sequence 272. App	Segmence 10227. A	Sequence 15. Appl	Sequence 338300.	Sequence 213115,
4 US-10-286-926-3	4 US-10-286-926-5	5 US-10-231-913-127	3 US-10-091-085-7	3 US-10-092-063-7	4 US-10-286-926-7		US-10-092-063-25		3 US-10-092-063-39		J US-09-925-299-876	1 US-10-369-493-6447	US-09-129-112-19	5 US-10-425-114-36762	4 US-10-369-493-2169	US-09-129-112-2	5 US-10-425-114-45875	US-09-129-112-9			US-10-369-493-1713								US-09-129-112-15	US-10-42	7
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14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

Sequence 27, Application US/10092063

Publication No. US20020173005A1

GeneRaL INFORMATION:
APPLICANT: Word, John
APPLICANT: Mulero, Julio
ITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
FILE REFERENCE: 28110/35908
CURRENT FILING DATE: 2002-03-05
FILE REPERENCE: 2007-03-05
FILE REPERENCE: 2007-03-05
FILE REPERENCE: 2007-03-05
FRIOR PRICE FILING DATE: 1999-07-05
FRIOR PELLOR NUMBER: 09/370,265
FRIOR PELLOR DATE: 1999-07-09
FRIOR FILING DATE: 1999-07-09
FRIOR FILING DATE: 1999-07-09
FRIOR FILING DATE: 1999-02-04
FRIOR PELLOR OWNER: 09/223,447
FRIOR PELLOR OWNER: 09/223,447
FRIOR PELLOR DATE: 1999-02-04
FRIOR PELLOR DATE: 1999-02-04
FRIOR FILING DATE: 1999-02-04
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FRIOR FILING DATE: 1999-07-05
FRIOR FILING DATE: 1999-07-06
FRIOR FILING DATE: 1999-07-06
FRIOR FILING DATE: 1999-07-06
FRIOR FILING DATE: 1999-07-16
; ORGANISM: Homo sapiens US-10-092-063-27 US-10-092-063-27 SEQ ID NO 27 LENGTH: 484 TYPE: PRT

Gaps 0 Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 8.7e-218;

Matches 456; Conservative 0; Mismatches 0; Indels 0;

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                                                                                                                                                                             29 MRXISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
                                                                                                  89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
                                                           SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
                                                                                                                                                                                                                                      FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
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APPLICANT: Ford, John
APPLICANT: Ford, John
APPLICANT: Wulero, Julio
APPLICANT: Weaug, George
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
FILE REPRENCE: 28110/3645/700N
CURRENT APPLICATION NUMBER: U5/481,286
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR PILING DATE: 2000-01-11
PRIOR PELLING DATE: 2000-01-11
PRIOR PILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR PILING DATE: 1999-07-16
PRIOR PLICATION NUMBER: 09/370,265
PRIOR PLICATION NUMBER: 09/37444
PRIOR FILING DATE: 1999-07-16
PRIOR PLICATION NUMBER: 09/12449
PRIOR FILING DATE: 1999-07-16
PRIOR PLICATION NUMBER: 09/118,205
PRIOR PLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR PLICATION NUMBER: 09/118,205
PRIOR PLICATION NUMBER: 09/118,205
PRIOR PLING DATE: 1998-07-16
PRIOR PLING DATE: 1999-07-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CRGANISM: Homo sapiens
US-10-286-926-27
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                                                                                                                                                                                                    61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
                                                                                                       1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
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Query Match
100.0%; Score 2364; DB 14; Length 484;
Best Local Similarity 100.0%; Pred. No. 8.7e-218;
Matches 456; Conservative 0; Mismatches 0; Indels 0;
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CURRENT APPLICATION NUMBER: US/10/231,913
PRIOR APPLICATION NUMBER: 06/251,660
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR PLING DATE: 2000-12-06
PRIOR PLING DATE: 2000-12-06
PRIOR PLING DATE: 2000-12-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patturajan, Meera
Shimkets, Richard A.
Casman, Stacle J.
Malyankar, Uriel M.
Tchernev, Velizar T.
Verner, Corine A.
Spytek, Kimberly A.
Shenoy, Suresh G.
Alsobrook II, John P.
Edinger, Schlomit
Peyman, John A.
Stone, David J.
Ellerman, Karen
Gangolli, Esha A.
Boldog, Ference L.
Colman, Steven D.
Eisen, Andrew J.
Liu, Xiaohong
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US-10-231-913-123
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Edinger, Schlomit
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PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-24
PRIOR PELING DATE: 2001-01-24
PRIOR PELING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR PILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR PILING DATE: 2001-04-24
PRIOR PILING DATE: 2001-08-20
PRIOR PILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR PILING DATE: 2001-08-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 123
LENGTH: 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Richard A.
APPLICANT: Analyankar, Uriel M.
APPLICANT: Tchernev, Velizar T.
APPLICANT: Tchernev, Velizar T.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0°
Best Local Similarity 100.0°
Matches 456; Conservative
                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-123
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61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
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                                APPLICANT: STUER, LOYAL O. APPLICANT: STUER, LOYAL O. APPLICANT: BIGNOGY, Ference L. APPLICANT: Boldog, Ference D. APPLICANT: Boldog, Ference D. APPLICANT: Boldog, Maralidhara APPLICANT: Boldogrub, Xiaohong APPLICANT: Spaderra, Steven M. APPLICANT: Spaderra, Steven D. TILLE REFRENCE: 21402-216

APPLICANT: Serhusen, Bryan D. TILLE REFRENCE: 21402-216

CURRENT FILING DATE: 2002-08-30

PRIOR APPLICATION NUMBER: 60/25,029

PRIOR APPLICATION NUMBER: 60/26,326

PRIOR PLING DATE: 2001-01-24

PRIOR PLING DATE: 2001-01-25

PRIOR PLING DATE: 2001-01-25

PRIOR PLING DATE: 2001-01-25

PRIOR PLING DATE: 2001-01-25

PRIOR PLING DATE: 2001-09-12

NUMBER OF SEQ ID NOS: 292

SOFTWARE: PALEATIN VET: 2.1
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Pred. No. 1.6e-217;
1; Mismatches 0;
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Peyman, John A.
Stone, David J.
Bllerman, Karen
Gangolli, Esha A.
Boldog, Ference L.
Colman, Steven D.
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Best Local Similarity 99.8%;
Matches 455; Conservative
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US-10-231-913-36
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269 IQASPPGYLTALRAMFNRTYKLYSYSYLGLGIMSARLAILGGVEGQPAKDGKELVSPCLSP 328
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241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
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                                                                           181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
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APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
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CURRENT FILING DATE: 2002-08-30
PRIOR PEDICATION NUMBER: 60/25,609
PRIOR PELING DATE: 2000-12-06
PRIOR PELING DATE: 2000-12-06
PRIOR PELING DATE: 2000-12-12
PRIOR PELING DATE: 2000-12-12
PRIOR PELING DATE: 2001-01-08
PRIOR PELING DATE: 2001-02-20
PRIOR PELING DATE: 2001-02-20
PRIOR PELING DATE: 2001-02-20
PRIOR PELING DATE: 2001-02-20
PRIOR PELING DATE: 2001-04-24
PRIOR PELING DATE: 2001-04-24
PRIOR PELING DATE: 2001-04-24
PRIOR PELING DATE: 2001-04-24
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PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
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Shimkets, Richard A.
Casman, Stacie J.
Malyankar, Uriel M.
Tchernev, Velizar T.
Vernet, Corine A.
Spytek, Kimberly A.
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Boldog, Ference L.
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Gangolli, Esha A.
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Eisen, Andrew J.
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APPLICANT: Serbusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR FILING DATE: 60/255,029
PRIOR FILING DATE: 2000-12-16
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR APPLICATION NUMBER: 60/260,942
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR PILING DATE: 2001-01-24
PRIOR PELING DATE: 2001-01-24
PRIOR PELING DATE: 2001-04-24
PRIOR PELING DATE: 2001-04-24
PRIOR PILING DATE: 2001-04-24
PRIOR PILING DATE: 2001-04-24
PRIOR PILING DATE: 2001-04-24
PRIOR PILING DATE: 2001-08-20
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99.6%; Pred. No. 4.1e-217;
tive 2; Mismatches 0;
               432 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 467
                                                                                                                                                                       Sequence 124, Application US/10231913 publication No. US20040005576A1 GENERAL INFORMATION:
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Spytek, Kimberly A.
Shenoy, Suresh G.
Alsobrook II, John P.
Bedinger, Schlomit
Peyman, John A.
Stone, David J.
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Padigaru, Muralidhara
Spaderna, Steven K.
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Shimkets, Richard A
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Tchernev, Velizar T
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Gangolli, Esha A.
Boldog, Ference L.
Colman, Steven D.
Eisen, Andrew J.
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Best Local Similarity 99.6
Matches 454; Conservative
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SEQ ID NO 124
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APPLICANT: Li, Li
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ORGANISM: Homo sapiens
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301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
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Best Local Similarity 86.6%; Pred. No. 5.7e-189;
Matches 394; Conservative 27; Mismatches 33;
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                        CURRENT APPLICATION NUMBER: US/10/231,9
CURRENT PILING DATE: 2002-08-30
PRIOR PELLICATION NUMBER: 60/251,660
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR PELLING DATE: 2000-12-06
PRIOR PELLING DATE: 2000-12-12
PRIOR PELLING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-24
PRIOR PELLING DATE: 2001-02-24
PRIOR PILING DATE: 2001-02-26
PRIOR PELLING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/266,183
PRIOR APPLICATION NUMBER: 60/266,183
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR PELLING DATE: 2001-04-24
PRIOR PELLING DATE: 2001-04-24
PRIOR PELLING DATE: 2001-08-20
PRIOR PELLING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
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Publication No. US20040005576A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Rattus norvegicus
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Best Local Similarity
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                                                                                                                                                                      38; Gaps
                                                                                                                         Query Match

89.5%; Score 2116; DB 15; Length 446;
Best Local Similarity 91.0%; Pred. No. 5.1e-194;
Matches 415; Conservative 1; Mismatches 2; Indels 38
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TITLE OF INVENTION: Proteins and Mucleic Acids Encoding Same
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Publication No. US20040005576Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                    29 MRKISNHGSLRVAV-----
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Spaderna, Steven K.
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; SOFTWARE: Patentin Ver. 2; SEQ ID NO 38; LENGTH: 446; TYPE: PRT; ORGANISM: Homo sapiens US-10-231-913-38
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85 TRVHVEQFT-RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLDVAKQDIPFDF 143
301 KGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRSKVLKLTRKID 360
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Pred. No. 1.5e-87;
2; Mismatches 133; Indels
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CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR APPLICATION NUMBER: 60/269,183
PRIOR APPLICATION NUMBER: 60/266,183
PRIOR PILING DATE: 2001-04-24
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/318,712
                                                                                                                                                                                                  Sequence 126, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
                                                431 NVETSWALGAIFHYIDSLN 449
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Tchernev, Velizar T.
Vernet, Corine A.
Spytek, Kimberly A.
Shenoy, Sureeh G.
Alsobrook II, John P.
Edinger, Schlomit
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                                                                          Steven K.
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Stone, David J.
Ellerman, Karen
Gangolli, Esha A.
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APPLICANT: Li, Li
APPLICANT: Patturajan, Meera
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Colman, Steven D
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US-10-231-913-126
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SEQ ID NO 126
LENGTH: 427
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Pred. No. 1.4e-178;
1; Mismatches 0; Indels 0:
                                                                                                                                                                                                                                                                                                               APPLICANT: Eisen, Andrew J.
APPLICANT: Liu, Xiaohong
APPLICANT: Dadigaru, Muralidhara
APPLICANT: Spaderna, Steven K.
APPLICANT: Schuusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REPERENCE: 21402-216
CURRENT PAPLICALING DATE: 2002-08-30
CURRENT PILING DATE: 2002-08-30
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PRIOR APPLICATION NUMBER: 60/251,660
PRIOR PILING DATE: 2000-12-02
PRIOR PILING DATE: 2000-12-12
PRIOR PILING DATE: 2000-12-12
PRIOR PILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-02-24
PRIOR PAPLICATION NUMBER: 60/269,942
PRIOR PILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-04-24
PRIOR PRIOR OF SEQ ID NOS: 292
                                                                                                                                        Alsobrook II, John P. Bdinger, Schlomit Peyman, John A. Stone, David J. Ellerman, Karen Gangolli, Bsha A. Boldog, Ference L. Colman, Steven D.
                                     Malyankar, Uriel M.
Tchernev, Velizar T.
                                                                            Vernet, Corine A.
Spytek, Kimberly A.
Shenoy, Suresh G.
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Best Local Similarity 99.7
Matches 378; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPILIHETFKAVKPGLSAYADD 120
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APPLICANT: Ford, John
APPLICANT: Ford, John
TILE OF INVENTION: MALEAC, JULIO
TILE OF INVENTION: MATERIALS RELATING TO NOVEL CD39-LIKE
TILE REFERENCE: S1110/35761
CURRENT APPLICATION NUMBER: 09/350,836
FRICA PILICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1999-07-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-02-04
PRIOR PRIOR PRIOR NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR PRIOR FILING DATE: 1999-02-04
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Publication No. US20020146772A1
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Best Local Similarity 52.4%;
Matches 204; Conservative 56
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                                                                                                  WKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT 203
                                                                                                                                                                                                                                                                                  204 INFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPGYLTALRMFNRTYKLYS 263
                                                                                                                                                                                                                                                                                                                                                                 179 VNFLTGQLHGRGQETVGTLDLGGASTQITFLPQFEKTLEQTPRGYLTSFEMFNSTFKLYT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 YSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQKAAAS 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 LHELCAARVSEVLONRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
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APPLICANT: Ford, John
APPLICANT: Ford, John
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/35/61
CURRENT PAPLICATION NUMBER: U5/10/091,085
FRIOR APPLICATION NUMBER: U5/20,0836
PRIOR APPLICATION NUMBER: 09/23,447
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1998-07-16
PRIOR FILING DATE: 1998-07-16
PRIOR FILING DATE: 1998-07-24
PRIOR FILING DATE: 1998-07-07-07
07
PRIOR FILING DATE: 1998-07-07-07-07
PRIOR FILING DATE: 1998-
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                                                                                                                                                        40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10091085
Publication No. US20020146772A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYIDSL 448
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Sequence 5, Application US/10092063

Sublication No. US2020133005A1

GENERAL INFORMATION:

APPLICANT: FOR CAT, John

APPLICANT: FOR CAT, John

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES

FILE REFERENCE: 28110/35908

CURRENT FILING DATE: 2002-03-05

PRIOR FILING DATE: 1999-07-16

PRIOR FILING DATE: 1999-07-16

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-04

PRIOR FILING DATE: 1998-07-04

PRIOR FILING DATE: 1998-07-04

PRIOR FILING DATE: 1998-07-16

PRIOR FILING DATE: 1998-07-24

PRIOR FILING DATE: 1998-07-24

PRIOR FILING DATE: 1998-07-24

PRIOR FILING DATE: 1998-07-26

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; Pred. No. 8.8e-87;
56; Mismatches 123; Indels
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US-10-286-926-3
US-10-286-926-3
Sequence 3, Application US/10286926
Publication No. US20030175752A1
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
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Best Local Similarity 52.44
Matches 204; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
CURRENT STILE OF INVENTIONS METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
FILE REFERENCE: 2810/35908
CURRENT FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-01-31
PRIOR PLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1999-07-04
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336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395
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                                                                        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL
                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10092063; Publication No. US20020173005A1; GENERAL INFORMATION:
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APPLICANT: Yeung, George
TILLE OF INVENTION: Methods and Materials Relating to CD39-Like
TILLE OF INVENTION: Polypeptides
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                              TITLE OF INVENTION: Methods and national control of ITLE OF INVENTION: Polypeptides
FILE REFERENCE: 28110/36457COM
CURRENT APPLICATION NUMBER: US/10/286,926
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR PLING DATE: 2000-01-11
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PRIOR PLING DATE: 1999-07-16
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US-10-286-926-3
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Sequence 5, Application US/10286926 Publication No. US20030175752A1 GENERAL INFORMATION: APPLICANT: FORG, John APPLICANT: Mulero, Julio APPLICANT: Yeung, George

US-10-286-926-5

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301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYDL 360
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              INVENTION: Methods and Materials Relating to CD39-Like
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Best Local Similarity 52.4%; Pred. No. 8.8e-87;
Matches 204; Conservative 56; Mismatches 123;
TITLE OF INVENTION: Methods and Materials Rel
TITLE OF INVENTION: Polypeptides,
FILE REPERENCE: 28110/36457CON
CURRENT APPLICATION NUMBER: US/10/286,926
CURRENT FILING DATE: 2002.11-01
PRIOR APPLICATION NUMBER: 09/55,800
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-13
PRIOR PILING DATE: 1990-09-16180
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-07-09
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PRIOR FILING DATE: 1998-07-04
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VALUER: 09/118,205
NUMBER OF SEQ ID NOS: 54
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US-10-286-926-5
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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7	US-09-608-285A-7	m	428	42.1	966	34
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GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240, 639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 2.0
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                         Sequence 2, Application US/09240639 Patent No. 6350447
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-09-240-639-2
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61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD

1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH

ò 셤 181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT

121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP

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301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL

AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS

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121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGIRLLPGEKAQKLLQKVKEVFKASP 180
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POTYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/10/107,660
CURRENT PILING DATE: 2002-03-27
PRIOR PILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE IIILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/905,744
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 09/240,639
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PRECEIT VET. 2.0
LENGTH: 456
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Pred. No. 1.1e-230;
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Best Local Similarity 100.
Matches 456; Conservative
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; ORGANISM: Homo sapiens
US-10-107-660-2
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CRGANISM: Homo sapiens
US-09-905-744-2
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Patent No. 6759214

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Frischauf, Anna Maria

TITLE OF INVENTION: ACIDS

FILE REPERENCE: 28110/36120E

CURRENT APPLICATION NUMBER: US/09/908,510A

CURRENT PILING DATE: 2001-07-13

PRIOR PILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-01-29

NUMBER: OF SEQ ID NOS: 32

SOFTWARE: Patentin version 3.1

SEQ ID NOS: 22
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          361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
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ORGANISM: Homo Sapiens
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, APPLICANT: Chadwick,
, APPLICANT: Frischau
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US-09-908-510A-2
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US-09-905-744-2
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US-09-905-732-2

Sequence 2, Application US/09905732

Sequence 2, Application US/09905732

Parent No. 6787328

APPLICANT: Chadwick, Brian Paul

APPLICANT: Frischauf, Anna-Maria

TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE

TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS

FILE REFERENCE: 9598-06

CURRENT FILING DATE: 2001-07-13

PRIOR FILING DATE: 1998-01-29

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATENTIN Ver. 2.0
                                                                              FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGT
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100.0%; Score 2364; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.1e-230;
Matches 456; Conservative 0; Mismatches 0; Indels 0
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING T
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/10/107,576
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US/09/240,639
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
          100.0%; Score 2364; DB 4;
100.0%; Pred. No. 1.1e-230;
tive 0; Mismatches 0;
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US-10-107-576-2
Sequence 2, Application US/10107576
Partent No. 6783959
GENERAL INFORMATION:
          Query Match
Best Local Similarity 100.
Matches 456; Conservative
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ORGANISM: Homo sapiens
US-10-107-576-2
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                                                                                                                                                    361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
                                                                                                                                                                                 389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448
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                                                                                            SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388
269 IQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328
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Patent No. 644771

GENERAL INFORMATION:

APPLICANT: Ford, John

APPLICANT: Ford, John

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE

TITLE OF INVENTION: POLYPEPTIDES

TITLE OF INVENTION: POLYPEPTIDES

TITLE OF INVENTION: POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/09/370,265

CURRENT APPLICATION NUMBER: US/09/370,265

CURRENT APPLICATION NUMBER: 09/350,836

EARLIER PILING DATE: 1999-07-16

EARLIER FILING DATE: 1999-07-16

EARLIER FILING DATE: 1999-07-09

EARLIER FILING DATE: 1999-07-09

EARLIER FILING DATE: 1999-07-09

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EARLIER PILING DATE: 1999-07-16
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                                                    SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYDDL
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                                                                                                                                                                                                                                                         KVLKLTRKIDNVETSWALGAIFHYIDSLNROKSPAS 456
                                                                                                                                                                                                                                                                                      449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484
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Best Local Similarity 100.
Matches 456; Conservative
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US-09-370-265-27
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                                  420
                                                               361 AAGYGLIDAEKGGSLVVGDFELAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
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APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TILLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570
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100.0%; Pred. No. 1.2e-230;
tive 0; Mismatches 0;
                                                                                                                                                                 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS
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CURRENT APPLICATION NUMBER: US/09/608,285A

CURRENT PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-25

PRIOR PLING DATE: 2000-04-25

PRIOR PILING DATE: 2000-01-11

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-13

PRIOR APPLICATION NUMBER: 09/481,238

PRIOR APPLICATION NUMBER: 09/31,265

PRIOR APPLICATION NUMBER: 09/31,265

PRIOR FILING DATE: 1999-07-16

PRIOR FILING DATE: 1999-07-16

PRIOR FILING DATE: 1999-07-16

PRIOR PILING DATE: 1999-07-19

PRIOR PILING DATE: 1999-07-19

PRIOR PILING DATE: 1999-07-19

PRIOR PILING DATE: 1999-07-19

PRIOR PILING DATE: 1999-07-19

PRIOR PILING DATE: 1999-07-14

PRIOR PILING DATE: 1999-07-14

PRIOR PILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/09608285A Patent No. 6335013
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US-09-608-285A-27
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SEQ ID NO 27
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Best Local S
Matches 456
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PACENTAL INCORMATION:
APPLICANT: Ford, John
APPLICANT: Ford, John
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
FILE REFERENCE: 28110/35908
CURRENT APPLICATION NUMBER: U$/09/370,628A
CURRENT PILING DATE: 1999-08-09
PRIOR PELING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: PQ1/S29/16180
PRIOR APPLICATION NUMBER: 09/550,836
PRIOR APPLICATION NUMBER: 09/513,447
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 27
                                                                                                                389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448
          LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
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                                                                                  361 AAGVGLIDABKGGSLVVGDFEIAAKYVCRTLETOPOSSPFSCMDLTYVSLLLQBFGFPRS
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Patent No. 6600032
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Matches 456; Conservative
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SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388
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                                                                               AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
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## APPLICANT: Mulero, Julio
## APPLICANT: Walero, Julio
## APPLICANT: Walero, Julio
## APPLICANT: Walero, Julio
## APPLICANT: Weing, George
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 28110/36457
CURRENT FILING DATE: 2000-04-25
## RIOR APPLICATION NUMBER: 09/481,238
## RIOR APPLICATION NUMBER: 09/370,265
## RIOR PILING DATE: 1999-00-09
## RIOR PILING DATE: 1999-07-16
## RIOR PILING DATE: 1999-07-16
## RIOR PILING DATE: 1999-07-16
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                                                                                                                                               KVLKLTRKIDNVETSWALGAIFHYIDSLNROKSPAS 456
                                                                                                                                                                                   449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484
                                                                                                                                                                                                                                                                                                                    Sequence 27, Application US/09557B00C Patent No. 6476211 GENERAL INFORMATION:
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Matches 456; Conservative
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; ORGANISM: Homo sapiens
US-09-557-800C-27
                                                   361
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US-09-608-285A-3
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              JS-09-608-285A-3
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SEQ ID NO 3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
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                                                    GENERAL INFORMATION:

APPLICANT: Ford, John
APPLICANT: MILEO, JULIO
APPLICANT: WILLER, JULIO
APPLICANT: WENG, GEORGE
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
TILE REFERENCE: 2810/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/557,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.7%; Score 2003; DB 3; Length 471; 98.5%; Pred. No. 4.6e-194; ive 1; Mismatches 5; Indels
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PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-03-19
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PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-07-24
PRIOR APPLICATION NUMBER: 09/12,449
PRIOR FILING DATE: 1999-07-24
PRIOR APPLICATION NUMBER: 09/12,449
PRIOR APPLICATION NUMBER: 09/12,449
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1998-07-16
                Sequence 60, Application US/09608285A Patent No. 6335013
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Matches 388; Conservative
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US-09-608-285A-60
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APPLICANI: MILLEO, UNITED
APPLICANI: MILLEO, ON UNITED
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLLYPEPTIDES
FILLS REFERENCE: 28110/36570
CURRENT PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/57,800
PRIOR FILING DATE: 2000-06-425
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
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52.4%; Pred. No. 2.2e-92;
ive 56; Mismatches 123; Indels
Sequence 3, Application US/09608285A Patent No. 6335013 GENERAL INFORMATION:
APPLICANT: Ford, John
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: PLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REPERENCE: 9588-066
CURRENT APPLICATION NUMBER: US/09/240,639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
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52.4%; Pred. No. 2.2e-92;
tive 56; Mismatches 123;
           396 STVLQLTKKVNNIETGWALGATFHLLQSL 424
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CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                     Sequence 6, Application US/09240639
Patent No. 6350447
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Patent No. 6350447
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Best Local Similarity 52.4%
Matches 204; Conservative
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US-09-240-639-6
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APPLICANT: FORG, Julio
APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
APPLICANT: Wulero, Julio
APPLICANT: Weing, George
ITTLE OF INVENTION: MCTHORS AND MATERIALS RELATING TO CD39-LIKE
ITILE OF INVENTION: POLYPEPTIDES
FILE REPRENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-36
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/310,265
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
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396 STVLQLTKKVNNIETGWALGATFHLLQSL 424
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                                                                                                                                  Sequence 5, Application US/09608285A
Patent No. 6335013
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ORGANISM: Homo sapiens
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SEQ ID NO 5
LENGTH: 428
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                                        Query Match 42.3%; Score 999; DB 3; Length 428; Best Local Similarity 52.4%; Pred. No. 2.2e-92; Matches 204; Conservative 56; Mismatches 123; Indels
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TYPE: PRT
// ORGANISM: Homo sapiens
US-09-240-639-9
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